GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 23433 Seconds
(without alignments)
17657.111 Million cell updates/sec

Title: US-09-275-883-1_COPY_1_8539
Perfect score: 8539
Sequence: 1 ctgacgcgccctgtagcggc.....atactacaacaccaccacct 8539

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8539	100.0	11282	6	BD203630	BD203630 Inducible
2	8539	100.0	11282	6	CQ790428	CQ790428 Sequence
3	8539	100.0	11282	6	AR342585	AR342585 Sequence
4	8539	100.0	11282	6	AX128601	AX128601 Sequence
5	8539	100.0	11282	6	AX174827	AX174827 Sequence
6	7657.2	89.7	13068	6	CQ790429	CQ790429 Sequence
7	7657.2	89.7	15081	6	CQ790448	CQ790448 Sequence
8	7657.2	89.7	17753	6	CQ790449	CQ790449 Sequence
9	7637.4	89.4	9951	6	AR282858	AR282858 Sequence
10	7637.4	89.4	9951	6	AX128602	AX128602 Sequence
11	7637.4	89.4	10524	6	AR282859	AR282859 Sequence
12	7637.4	89.4	11927	6	AR282860	AR282860 Sequence
13	7637.4	89.4	13905	6	AR137241	AR137241 Sequence
14	7637.4	89.4	13905	6	AR282856	AR282856 Sequence
15	7634.8	89.4	8000	6	AR221249	AR221249 Sequence
16	7634.8	89.4	8000	6	AR230676	AR230676 Sequence
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18	7634.8	89.4	8000	6	AR237760	AR237760 Sequence
19	7634.8	89.4	8000	6	AR353270	AR353270 Sequence
20	7634.8	89.4	8000	6	BD078844	BD078844 Recombine
21	7634.8	89.4	8000	6	BD085671	BD085671 Recombina
22	7634.8	89.4	11703	14	SINCG	J02363 Sindbis vir
23	7634.8	89.4	11740	6	AR221250	AR221250 Sequence
24	7634.8	89.4	11740	6	AR230677	AR230677 Sequence
25	7634.8	89.4	11740	6	AR234151	AR234151 Sequence
26	7634.8	89.4	11740	6	AR237761	AR237761 Sequence
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29	7634.8	89.4	11740	6	BD085672	BD085672 Recombina
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31	7620.4	89.2	11703	6	BD269911	BD269911 Compositi
32	7618.8	89.2	11703	6	AR042412	AR042412 Sequence
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37	7617.2	89.2	8000	6	AR230675	AR230675 Sequence
38	7617.2	89.2	8000	6	AR234149	AR234149 Sequence
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43	7612.4	89.1	16656	6	AR020969	AR020969 Sequence
44	7612.4	89.1	16656	6	AR043384	AR043384 Sequence
45	7612.4	89.1	16656	6	AR062299	AR062299 Sequence

ALIGNMENTS

RESULT 1
BD203630
LOCUS BD203630 11282 bp DNA linear PAT 17-JUL-2003
DEFINITION Inducible alpha virus gene expression system.
ACCESSION BD203630
VERSION BD203630.1 GI:33013400
KEYWORDS JP 2002509729-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 11282)
AUTHORS Renner,W.A., Nieba,L. and Boorsma,M.
TITLE Inducible alpha virus gene expression system
JOURNAL Patent: JP 2002509729-A 1 02-APR-2002;
CYTOS BIOTECHNOLOGY AG
COMMENT OS Artificial Sequence
PN JP 2002509729-A/1
PD 02-APR-2002
PF 25-MAR-1999 JP 2000541320
PR 27-MAR-1998 US 60/079562
PI WOLFGANG A RENNER,LARS NIEBA,MARCO BOORSMA
PC C12N15/09,A01K67/027,A61K48/00,C07K14/18,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N5/10,C12N7/04,C12N9/12,C12N15/00,C12N5/00 CC Description of Artificial Sequence:cDNA
FH Key Location/Qualifiers
FT source 1. .11282
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .11282
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 100.0%; Score 8539; DB 6; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

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Qy        61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
Db        61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy       121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
Db       121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180

Qy       181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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Qy       241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
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Qy       301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
Db       301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360

Qy       361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
Db       361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420

Qy       421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480
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Qy       481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540
Db       481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540

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Db       781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840

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Db       841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900

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Db       901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960

Qy       961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
Db       961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020

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Db      1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080

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Db      1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140
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Db      1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320

Qy      1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380
Db      1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380

Qy      1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440
Db      1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440

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Db      1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500

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Db      1621 GGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTTATTTCTCC 1680

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Qy      1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800
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Qy      1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920
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Db      2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
Qy      2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
Db      2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
Qy      2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
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Qy      2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
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Qy      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
Db      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
Qy      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
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Qy      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
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Qy      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
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Qy      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
Db      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800

Qy      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
Db      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860

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Qy      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980

Qy      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
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Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
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Db      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220

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Db      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400

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Qy      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
Db      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000

Qy      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
Db      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060

Qy      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
Db      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120

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Qy      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
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Qy       7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
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Db       8521 TACTACAACACCACCACCT 8539
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RESULT 2
CQ790428

LOCUS	CQ790428	11282 bp DNA linear PAT 29-MAR-2004
DEFINITION	Sequence 1 from Patent WO2004018506.	
ACCESSION	CQ790428	
VERSION	CQ790428.1 GI:45823470	
KEYWORDS	.	
SOURCE	synthetic construct	
ORGANISM	synthetic construct	
	other sequences; artificial sequences.	
REFERENCE	1	
AUTHORS	Ivanova,L., Renner,W.A. and Saudan,P.	
TITLE	Inducible alphaviral/orip based gene expression system	
JOURNAL	Patent: WO 2004018506-A 1 04-MAR-2004;	

Cytos Biotechnology AG (CH)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="cDNA"
ORIGIN

Query Match 100.0%; Score 8539; DB 6; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
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Db        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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Qy       1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
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Qy      2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
Db      2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
Qy      2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
Db      2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
Qy      2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
Db      2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
Qy      2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280
Db      2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280
Qy      2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
Db      2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
Qy      2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
Db      2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
Qy      2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
Db      2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
Qy      2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
Db      2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
Qy      2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
Db      2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
Qy      2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
Db      2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
Qy      2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
Db      2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
Qy      2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
Db      2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
Qy      2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
Db      2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
Qy      2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
Db      2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
Qy      2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
Db      2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
Qy      2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
Db      2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
Qy      3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
Db      3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
Qy      3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
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Db      3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
Qy      3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Db      3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Qy      3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Db      3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Qy      3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
Db      3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
Qy      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Db      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Qy      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Db      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Qy      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Db      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Qy      3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Db      3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Qy      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Db      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Qy      3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Db      3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Qy      3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
Db      3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
Qy      3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
Db      3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
Qy      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Db      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Qy      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Db      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Qy      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Db      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Qy      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Db      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Qy      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Db      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Qy      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
Db      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
Qy      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
Db      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
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Qy      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260

Qy      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320

Qy      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380

Qy      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440

Qy      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500

Qy      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560

Qy      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620

Qy      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680

Qy      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740

Qy      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800

Qy      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860

Qy      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920

Qy      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980

Qy      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040

Qy      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100

Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160

Qy      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220

Qy      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
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Qy      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340

Qy      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400

Qy      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460

Qy      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520

Qy      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580

Qy      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640

Qy      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700

Qy      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760

Qy      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820

Qy      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880

Qy      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940

Qy      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000

Qy      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060

Qy      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120

Qy      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180

Qy      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240

Qy      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300

Qy      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360

Qy      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
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Db      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
Qy      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
Db      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
Qy      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
Db      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
Qy      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
Db      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
Qy      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
Db      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
Qy      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
Db      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
Qy      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
Db      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
Qy      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
Db      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
Qy      6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
Db      6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
Qy      6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Db      6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Qy      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Db      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Qy      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Db      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Qy      7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
Db      7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
Qy      7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
Db      7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
Qy      7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
Db      7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
Qy      7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
Db      7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
Qy      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Db      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Qy      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Db      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Qy      7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
Db      7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
Qy      7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
Db      7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
Qy      7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
Db      7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
Qy      7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Db      7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Qy      7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Db      7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Qy      7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Db      7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Qy      7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
Db      7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
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Db      8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
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Db      8521 TACTACAACACCACCACCT 8539
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RESULT 3
AR342585
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DEFINITION  Sequence 1 from patent US 6576443.
ACCESSION   AR342585
VERSION     AR342585.1  GI:33737767
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11282)
  AUTHORS   Hennecke,F. and Renner,W.A.
  TITLE     Replicon based activation of endogenous genes
  JOURNAL   Patent: US 6576443-A 1 10-JUN-2003;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 8539;  DB 6;  Length 11282;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 8539;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
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Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
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Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
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Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Qy       1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860
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Qy       3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
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Qy       3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
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Qy       3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
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Qy       3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Db       3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420

Qy       3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Db       3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480

Qy       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
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Qy       3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
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Qy       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
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Qy       3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
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Qy       3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
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Db      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
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Db      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Qy      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
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Qy      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
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Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
Qy      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
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Db      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
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Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
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Db      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
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RESULT 4
AX128601
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DEFINITION  Sequence 1 from Patent WO0130989.
ACCESSION   AX128601
VERSION     AX128601.1  GI:14135063
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Renner,W.A. and Nieba,L.
  TITLE     Method for creating divergent populations of nucleic acid molecules
            and proteins
  JOURNAL   Patent: WO 0130989-A 1 03-MAY-2001;
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ORIGIN

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  Matches 8539;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980
Qy       1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040
Qy       2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
Qy       2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
Qy       2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
Qy       2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280
Qy       2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
Qy       2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
Qy       2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
Qy       2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
Qy       2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
Qy       2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
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Qy       2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
Qy       2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
Qy       2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
Qy       2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
Qy       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
Qy       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
Qy       3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
Qy       3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
Qy       3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Qy       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Qy       3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
Qy       3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Qy       3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Qy       3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Qy       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Qy       3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Qy       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Qy       3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
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Qy       3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780

Qy       3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840

Qy       3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900

Qy       3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960

Qy       3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020

Qy       4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080

Qy       4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140

Qy       4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200

Qy       4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260

Qy       4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320

Qy       4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380

Qy       4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440

Qy       4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500

Qy       4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560

Qy       4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620

Qy       4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680

Qy       4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740

Qy       4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800

Qy       4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860

Qy       4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920

Qy       4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980

Qy       4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040

Qy       5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100

Qy       5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160

Qy       5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220

Qy       5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280

Qy       5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340

Qy       5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400

Qy       5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460

Qy       5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520

Qy       5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580

Qy       5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640

Qy       5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
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Db       5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700

Qy       5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760

Qy       5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820

Qy       5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880

Qy       5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
Qy       5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
Qy       6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
Qy       6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
Qy       6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
Qy       6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
Qy       6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
Qy       6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
Qy       6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
Qy       6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
Qy       6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
Qy       6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
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Qy       6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
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Qy       6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
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Qy       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
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Db       8521 TACTACAACACCACCACCT 8539
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RESULT 5
AX174827

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LOCUS       AX174827               11282 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 1 from Patent WO0142442.
ACCESSION   AX174827
VERSION     AX174827.1  GI:14598323
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Hennecke,F. and Renner,W.A.
  TITLE     Activation of endogenous genes by genomic introduction of a
            replicon
  JOURNAL   Patent: WO 0142442-A 1 14-JUN-2001;
            Cytos Biotechnology AG (CH)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="pCYTts"
ORIGIN
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Query Match 100.0%; Score 8539; DB 6; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
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Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
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Qy        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960
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Db        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960

Qy        961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
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Db      2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
Qy      2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
Db      2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
Qy      3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
Db      3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
Qy      3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
Db      3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
Qy      3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Db      3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Qy      3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Db      3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Qy      3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
Db      3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
Qy      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Db      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Qy      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Db      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Qy      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Db      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
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Qy       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540

Qy       3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600

Qy       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660

Qy       3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720

Qy       3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780

Qy       3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840

Qy       3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900

Qy       3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960

Qy       3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020

Qy       4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080

Qy       4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140

Qy       4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200

Qy       4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260

Qy       4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320

Qy       4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380

Qy       4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440

Qy       4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500

Qy       4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560

Qy       4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620

Qy       4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680

Qy       4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740

Qy       4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800

Qy       4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860

Qy       4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920

Qy       4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980

Qy       4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040

Qy       5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100

Qy       5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160

Qy       5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220

Qy       5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280

Qy       5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340

Qy       5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400

Qy       5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460

Qy       5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520

Qy       5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580

Qy       5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640

Qy       5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
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Db      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
Qy      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
Db      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
Qy      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
Db      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
Qy      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
Db      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
Qy      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
Db      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
Qy      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
Db      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
Qy      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
Db      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
Qy      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
Db      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
Qy      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
Db      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
Qy      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
Db      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
Qy      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
Db      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
Qy      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
Db      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
Qy      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
Db      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
Qy      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
Db      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
Qy      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
Db      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
Qy      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
Db      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
Qy      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
Db      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
Qy      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
Db      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
Qy      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
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Db      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
Qy      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
Db      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
Qy      6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
Db      6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
Qy      6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Db      6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Qy      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Db      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Qy      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Db      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Qy      7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
Db      7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
Qy      7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
Db      7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
Qy      7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
Db      7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
Qy      7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
Db      7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
Qy      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Db      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Qy      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Db      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Qy      7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
Db      7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
Qy      7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
Db      7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
Qy      7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
Db      7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
Qy      7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Db      7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Qy      7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Db      7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Qy      7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Db      7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Qy      7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
Db      7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
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Qy       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920

Qy       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980

Qy       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040

Qy       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100

Qy       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160

Qy       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220

Qy       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280

Qy       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340

Qy       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400

Qy       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
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RESULT 6
CQ790429
LOCUS       CQ790429               13068 bp    DNA     linear   PAT 29-MAR-2004
DEFINITION  Sequence 2 from Patent WO2004018506.
ACCESSION   CQ790429
VERSION     CQ790429.1  GI:45823471
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ivanova,L., Renner,W.A. and Saudan,P.
  TITLE     Inducible alphaviral/orip based gene expression system
  JOURNAL   Patent: WO 2004018506-A 2 04-MAR-2004;
            Cytos Biotechnology AG (CH)
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 89.7%; Score 7657.2; DB 6; Length 13068;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7642; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
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Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
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Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
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Db      5669 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5728

Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
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Db      5729 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5788

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Qy      6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 7
CQ790448
LOCUS       CQ790448               15081 bp    DNA     linear   PAT 29-MAR-2004
DEFINITION  Sequence 21 from Patent WO2004018506.
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VERSION     CQ790448.1  GI:45823490
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ivanova,L., Renner,W.A. and Saudan,P.
  TITLE     Inducible alphaviral/orip based gene expression system
  JOURNAL   Patent: WO 2004018506-A 21 04-MAR-2004;
            Cytos Biotechnology AG (CH)
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ORIGIN

  Query Match             89.7%;  Score 7657.2;  DB 6;  Length 15081;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7642;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
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Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db      3689 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3748
Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
Db      3749 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3808
Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
Db      3809 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCTCACTAACA 3868
Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
Db      3869 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3928
Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
Db      3929 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3988
Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
Db      3989 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4048
Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
Db      4049 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4108
Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
Db      4109 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4168
Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
Db      4169 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4228
Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
Db      4229 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4288
Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
Db      4289 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4348
Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
Db      4349 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4408
Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
Db      4409 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCGAAAAATTCTTGAACCAGTTCA 4468
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Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
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Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db      4649 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4708
Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
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Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
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Db      4769 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4828

Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
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Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
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Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
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Db      4949 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5008

Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
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Db      5009 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5068

Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5069 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5128

Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
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Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
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Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
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Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
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Db      5309 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5368

Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5369 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5428

Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
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Db      5429 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5488

Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
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Db      5489 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5548

Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
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Db      5549 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5608

Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5609 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5668

Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5669 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5728

Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5729 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5788

Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
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Qy      5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
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Qy      5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
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Qy      5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
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Db      5969 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6028

Qy      6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6029 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6088

Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
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Db      6149 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6208

Qy      6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6209 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6268

Qy      6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6269 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6328

Qy      6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6329 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6388

Qy      6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
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Db      6389 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6448

Qy      6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
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Qy      6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
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Qy      6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
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Db      6929 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6988
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Qy      7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
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RESULT 8

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CQ790449
LOCUS       CQ790449               17753 bp    DNA     linear   PAT 29-MAR-2004
DEFINITION  Sequence 22 from Patent WO2004018506.
ACCESSION   CQ790449
VERSION     CQ790449.1  GI:45823491
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ivanova,L., Renner,W.A. and Saudan,P.
  TITLE     Inducible alphaviral/orip based gene expression system
  JOURNAL   Patent: WO 2004018506-A 22 04-MAR-2004;
            Cytos Biotechnology AG (CH)
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                     /mol_type="unassigned DNA"
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                     /note="cDNA"
ORIGIN

  Query Match             89.7%;  Score 7657.2;  DB 6;  Length 17753;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7642;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928
Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
Db        929 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 988
Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
Db        989 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1048
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Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
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Db       1049 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1108

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
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Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
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Db       1229 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1288

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1348

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1408

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1468

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1469 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1528

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1529 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1588

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1589 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1648

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1649 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1708

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1709 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1768

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1769 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1828

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1829 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1888

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1889 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1948

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1949 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2008

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2009 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2068

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2069 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2128
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Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2129 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2188

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2189 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2248

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2249 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2308

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2309 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2368

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2369 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2428

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2429 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2488

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2489 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2548

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2549 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2608

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2609 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2668

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2669 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2728

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2729 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2788

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2789 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2848

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2849 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2908

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2909 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2968

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2969 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3028

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3029 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3088

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3089 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3148

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3149 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3208

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
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Db      3209 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3268
Qy      3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
Db      3269 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3328
Qy      3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
Db      3329 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3388
Qy      3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
Db      3389 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3448
Qy      3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
Db      3449 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3508
Qy      3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
Db      3509 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3568
Qy      3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
Db      3569 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3628
Qy      3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
Db      3629 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3688
Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db      3689 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3748
Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
Db      3749 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3808
Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
Db      3809 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCTCACTAACA 3868
Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
Db      3869 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3928
Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
Db      3929 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3988
Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
Db      3989 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4048
Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
Db      4049 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4108
Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
Db      4109 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4168
Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
Db      4169 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4228
Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
Db      4229 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4288
Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
Db      4289 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4348
Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
Db      4349 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4408
Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
Db      4409 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCGAAAAATTCTTGAACCAGTTCA 4468
Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
Db      4469 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4528
Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
Db      4529 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4588
Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
Db      4589 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4648
Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db      4649 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4708
Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
Db      4709 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4768
Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
Db      4769 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4828
Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
Db      4829 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4888
Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
Db      4889 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4948
Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
Db      4949 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5008
Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
Db      5009 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5068
Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
Db      5069 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5128
Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
Db      5129 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5188
Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
Db      5189 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5248
Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db      5249 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5308
Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
Db      5309 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5368
Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
Db      5369 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5428
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Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5429 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5488

Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5489 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5548

Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5549 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5608

Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5609 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5668

Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5669 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5728

Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5729 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5788

Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5789 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5848

Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5849 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5908

Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5909 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5968

Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5969 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6028

Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6029 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6088

Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6089 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6148

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6149 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6208

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6209 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6268

Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6269 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6328

Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6329 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6388

Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6389 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6448

Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6449 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6508
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Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6509 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6568

Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
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Db       6569 CTCTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6628

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
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Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6749 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6808

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6809 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6868

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
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Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
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Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
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Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
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Db       7109 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7168

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
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Db       7169 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7228

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
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Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
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Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
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Db       7349 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7408

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
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Db       7409 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7468

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
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Db       7469 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7528

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
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Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
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Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
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Db       7709 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7768

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Db       7769 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7828

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
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Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
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Db       7889 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7948

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
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Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Db       8009 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8068

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
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Db       8069 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8128

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
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Db       8129 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8188

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
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Db       8189 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8248

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
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Db       8249 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8308

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
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Db       8309 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8368

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
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Db       8369 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8428

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
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Db       8429 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8488

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
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Db       8489 CTGACTAATACCACAACACCACCACCT 8515


RESULT 9
AR282858
LOCUS       AR282858               9951 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 3 from patent US 6524792.
ACCESSION   AR282858
VERSION     AR282858.1  GI:29719660
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 9951)
  AUTHORS   Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
  TITLE     Expression cloning processes for the discovery, characterization
            and isolation of genes encoding polypeptides with a predetermined
            property
  JOURNAL   Patent: US 6524792-A 3 25-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .9951
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.4%;  Score 7637.4;  DB 6;  Length 9951;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
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Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

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Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
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Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
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Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
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Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
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Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
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Qy      1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
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Db       841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy      1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
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Db       901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy      1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy      1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
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Qy      1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
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Qy      2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
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Qy      2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
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Db      1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy      2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
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Db      1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy      2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
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Db      1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy      2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
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Qy      2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
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Qy      2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
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Db      1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy      2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
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Db      1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy      2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
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Db      1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy      2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
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Db      1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy      2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
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Qy      2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
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Qy      2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
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Qy      2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
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Qy      3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
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Qy      3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
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Db      2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy      3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
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Db      2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

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Db      2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

Qy      3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy      3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy      3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy      3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy      3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy      3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy      3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980
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Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy       4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy       4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy       4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780

Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy       4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             |||||||  | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy       4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260

Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380

Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500

Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800

Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860

Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920

Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980

Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040

Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100

Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160

Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220
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Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
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Db       5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400

Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460

Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520

Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580

Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640

Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700

Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||| ||||
Db       6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780

Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
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RESULT 10
AX128602
LOCUS       AX128602               9951 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2 from Patent WO0130989.
ACCESSION   AX128602
VERSION     AX128602.1  GI:14135064
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Renner,W.A. and Nieba,L.
  TITLE     Method for creating divergent populations of nucleic acid molecules
            and proteins
  JOURNAL   Patent: WO 0130989-A 2 03-MAY-2001;
            Cytos Biotechnology AG (CH) ; Renner, Wolfgand Andreas (CH) ;
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ORIGIN

  Query Match             89.4%;  Score 7637.4;  DB 6;  Length 9951;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
Db      3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540
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Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
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Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
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Db      4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
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Db      4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500

Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
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Db      4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
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Db      4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
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Db      4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
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Db      4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
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Db      4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860

Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
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Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
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Db      4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980

Qy      5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040

Qy      5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
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Db      5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100

Qy      5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
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Qy      6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
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Db      5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220

Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
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Db      5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy      6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
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Db      5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340

Qy      6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
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Db      5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400

Qy      6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
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Qy      6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
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Qy      6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
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Qy      6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
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Qy      6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
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Db      5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700

Qy      6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
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Qy      6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
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Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880

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Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
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Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

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Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
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Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
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Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
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Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
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Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
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Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
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Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
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Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
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Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
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Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
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Db       7621 CTGACTAATACTACAACACCACCACCT 7647
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RESULT 11
AR282859
LOCUS       AR282859               10524 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 4 from patent US 6524792.
ACCESSION   AR282859
VERSION     AR282859.1  GI:29719661
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10524)
  AUTHORS   Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
  TITLE     Expression cloning processes for the discovery, characterization
            and isolation of genes encoding polypeptides with a predetermined
            property
  JOURNAL   Patent: US 6524792-A 4 25-FEB-2003;
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match            89.4%;  Score 7637.4;  DB 6;  Length 10524;
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Db         1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy       953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Db        61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
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Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
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Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
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Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
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Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
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Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
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Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
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Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
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Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
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Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
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Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
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Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
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Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
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Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160
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Qy      3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220

Qy      3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy      3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy      3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

Qy      3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy      3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy      3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy      3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy      3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy      3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy      3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240
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Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780

Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             |||||||  | ||| ||||||||||||||||||||||||||||||||||||||||||||
Db      3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260

Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
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Db      4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380
Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db      4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440
Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
Db      4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500
Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
Db      4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560
Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
Db      4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620
Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
Db      4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680
Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
Db      4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740
Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
Db      4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800
Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
Db      4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860
Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db      4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920
Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
Db      4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980
Qy      5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
Db      4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040
Qy      5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
Db      5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100
Qy      5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
Db      5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160
Qy      6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
Db      5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220
Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
Db      5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280
Qy      6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
Db      5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340
Qy      6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
Db      5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400
Qy      6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
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Db      5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460
Qy      6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
Db      5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520
Qy      6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
Db      5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580
Qy      6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
Db      5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640
Qy      6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
Db      5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
Qy      6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
Db      5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760
Qy      6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
Db      5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820
Qy      6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
Db      5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880
Qy      6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
Db      5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940
Qy      6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
Db      5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000
Qy      6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
Db      6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060
Qy      6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
Db      6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120
Qy      7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
Db      6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180
Qy      7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
Db      6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240
Qy      7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
Db      6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300
Qy      7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
Db      6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360
Qy      7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
Db      6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420
Qy      7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
Db      6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480
Qy      7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
Db      6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540
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Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
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Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
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Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
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Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
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Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
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Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
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Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
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Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
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Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
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Db       7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
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Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
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Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
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Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
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Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
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Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
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Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
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Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620
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Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
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Db       7621 CTGACTAATACTACAACACCACCACCT 7647


RESULT 12
AR282860
LOCUS       AR282860               11927 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6524792.
ACCESSION   AR282860
VERSION     AR282860.1  GI:29719662
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11927)
  AUTHORS   Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
  TITLE     Expression cloning processes for the discovery, characterization
            and isolation of genes encoding polypeptides with a predetermined
            property
  JOURNAL   Patent: US 6524792-A 5 25-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .11927
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.4%;  Score 7637.4;  DB 6;  Length 11927;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
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Db         481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
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Db         541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
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Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660
Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720
Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780
Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840
Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
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Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
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Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020
Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080
Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140
Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
Db       1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200
Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
Db       1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260
Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320
Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380
Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440
Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
Db       1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500
Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560
Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620
Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
Db       1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680
Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
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Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
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Db       1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980
Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
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Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
Db       2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100
Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
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Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
Db       2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340
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Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
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Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
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Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
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Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             |||||||  | ||| ||||||||||||||||||||||||||||||||||||||||||||
Db      3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
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Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
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Db      4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
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Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
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Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220
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Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
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Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
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RESULT 13
AR137241
LOCUS AR137241 13905 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6197502.
ACCESSION AR137241
VERSION AR137241.1 GI:14478750
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 13905)
AUTHORS Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
TITLE Expression cloning processes for the discovery characterization, and isolation of genes encoding polypeptides with a predetermined property
JOURNAL Patent: US 6197502-A 1 06-MAR-2001;
FEATURES Location/Qualifiers
source 1. .13905
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 89.4%; Score 7637.4; DB 6; Length 13905;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
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Qy      2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy      2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500

Qy      2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy      2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy      2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy      2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy      2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800

Qy      2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860

Qy      2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920

Qy      2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980

Qy      2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy      2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy      2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160

Qy      3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220

Qy      3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy      3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy      3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400
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Qy      3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy      3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy      3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy      3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy      3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy      3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy      3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTTCTAAAC 3300

Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
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Db       3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540
Qy       4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
Db       3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600
Qy       4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
Db       3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660
Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
Db       3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720
Qy       4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
Db       3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780
Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db       3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840
Qy       4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
Db       3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900
Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
Db       3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960
Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
Db       3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020
Qy       4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
Db       4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080
Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
Db       4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140
Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
Db       4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200
Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
Db       4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260
Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
Db       4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320
Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
Db       4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380
Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db       4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440
Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
Db       4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500
Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
Db       4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560
Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
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Db       4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620
Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
Db       4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680
Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
Db       4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740
Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
Db       4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800
Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
Db       4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860
Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db       4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920
Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
Db       4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980
Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
Db       4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040
Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
Db       5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100
Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
Db       5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160
Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
Db       5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220
Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
Db       5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280
Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
Db       5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340
Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
Db       5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400
Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
Db       5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460
Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
Db       5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520
Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
Db       5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580
Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
Db       5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640
Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
Db       5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
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Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             |||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||||
Db       6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
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Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
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Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
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Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
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Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
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Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
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Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
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Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
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Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
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Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
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Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
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Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
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Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
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Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
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Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
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Db       7621 CTGACTAATACTACAACACCACCACCT 7647
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RESULT 14
AR282856

LOCUS	AR282856	13905 bp DNA linear PAT 10-APR-2003
DEFINITION	Sequence 1 from patent US 6524792.	
ACCESSION	AR282856	
VERSION	AR282856.1 GI:29719658	
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unknown.	
	Unclassified.	
REFERENCE	1 (bases 1 to 13905)	
AUTHORS	Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.	

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  TITLE     Expression cloning processes for the discovery, characterization
            and isolation of genes encoding polypeptides with a predetermined
            property
  JOURNAL   Patent: US 6524792-A 1 25-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .13905
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.4%;  Score 7637.4;  DB 6;  Length 13905;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
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Db         361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
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Db         481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
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Db         541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
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Db         601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
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Db         721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
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Db         781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
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Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
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Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
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Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
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Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
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Db         1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
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Db         1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
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Db         1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
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Db         1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
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Db         1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
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Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
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Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
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Db       2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
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Db       2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
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Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
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Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
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Db       2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
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Db       3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy       4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
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Db       3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy       4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy       4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780

Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy       4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             |||||||  | ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy       4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
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Db       4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

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Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
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Db       4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380

Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
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Db       4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
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Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
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Db       4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
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Db       4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
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Db       4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
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Db       4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
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Db       4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800

Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
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Db       4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860

Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
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Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
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Db       4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980

Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040

Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
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Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
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Db       5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160

Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
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Db       5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220

Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
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Db       5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
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Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
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Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
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Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
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Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
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Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
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Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
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Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180

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Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAAACATGAGTATA 7192
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Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
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Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
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RESULT 15
AR221249

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LOCUS       AR221249               8000 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 102 from patent US 6426196.
ACCESSION   AR221249
VERSION     AR221249.1  GI:23328145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 8000)
  AUTHORS   Dubensky,T.W. Jr., Polo,J.M., Schlesinger,S. and Frolov,I.
  TITLE     Alphavirus structural protein expression cassettes
  JOURNAL   Patent: US 6426196-A 102 30-JUL-2002;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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Query Match 89.4%; Score 7634.8; DB 6; Length 8000;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7639; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
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Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
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Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
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Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540
Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600
Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660
Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720
Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780
Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840
Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900
Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960
Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020
Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080
Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140
Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
Db       1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200
Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
Db       1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260
Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320
Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380
Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440
Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
Db       1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500
Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560
Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
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Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620
Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
Db       1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680
Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
Db       1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740
Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
Db       1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800
Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
Db       1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860
Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
Db       1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920
Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
Db       1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980
Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
Db       1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040
Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
Db       2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100
Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
Db       2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160
Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
Db       2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220
Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
Db       2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280
Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
Db       2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340
Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
Db       2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400
Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
Db       2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460
Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
Db       2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520
Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
Db       2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580
Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
Db       2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640
Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
Db       2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700
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Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy       4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy       4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy       4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780
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Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy       4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             |||||||  | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy       4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260

Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380

Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500

Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 ATGAGTTAGTATGGATCCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800

Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860

Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
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Db       4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920
Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
Db       4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980
Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
Db       4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040
Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
Db       5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100
Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
Db       5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160
Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
Db       5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220
Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
Db       5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280
Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
Db       5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340
Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
Db       5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400
Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
Db       5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460
Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
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Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
Db       5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580
Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
Db       5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640
Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
Db       5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
Db       5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760
Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820
Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880
Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940
Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000
Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060
Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
Db       6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120
Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180
Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
Db       6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240
Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300
Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360
Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420
Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480
Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540
Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
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Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660
Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720
Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840
Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
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Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
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Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
Db       7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080
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Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140

Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
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Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
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Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

Qy       8513 CTGACTAATACTACAACACCACCACC 8538
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Db       7621 CTGACTAATACTACAACACCACCACC 7646
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Search completed: March 23, 2005, 23:36:38
Job time : 23457 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 16275 Seconds
(without alignments)
19971.170 Million cell updates/sec

Title: US-09-275-883-1_COPY_1_8539
Perfect score: 8539
Sequence: 1 ctgacgcgccctgtagcggc.....atactacaacaccaccacct 8539

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	616.8	7.2	813	7	CN385673	CN385673 LE2TR04D2
c 2	616.8	7.2	860	7	CV089193	CV089193 est_c_vir
c 3	616.8	7.2	862	7	CN385663	CN385663 LE2TR04D1
c 4	616.8	7.2	874	7	CN385637	CN385637 LE2TR04C0
c 5	616.8	7.2	884	7	CN385877	CN385877 LE2TR04M1
c 6	616.8	7.2	899	7	CN385574	CN385574 LE2TR03P1
c 7	616.8	7.2	921	7	CN384456	CN384456 LE2TR01A0
c 8	608.8	7.1	805	2	BE421195	BE421195 HWM006.G0
c 9	607.8	7.1	685	5	BU724260	BU724260 SJMBFC05
c 10	607.8	7.1	702	6	CB549906	CB549906 MMPL0007_
c 11	607.8	7.1	714	6	CB548528	CB548528 MMPL0022_
c 12	607.8	7.1	753	5	BQ157858	BQ157858 NF103A09P
c 13	607.8	7.1	758	5	BQ158943	BQ158943 NF095D07P
c 14	607.8	7.1	764	5	BQ158750	BQ158750 NF070F07P
c 15	607.8	7.1	771	5	BQ158875	BQ158875 NF076G06P
c 16	607.8	7.1	773	5	BQ156760	BQ156760 NF096H04I
c 17	607.8	7.1	774	5	BQ158974	BQ158974 NF098A06P
c 18	607.8	7.1	775	5	BQ158844	BQ158844 NF073D03P
c 19	607.8	7.1	776	5	BQ159296	BQ159296 NF092H12P
c 20	607.8	7.1	779	5	BQ158936	BQ158936 NF083H10P
c 21	607.8	7.1	782	5	BQ158981	BQ158981 NF099E10P
c 22	607.8	7.1	794	5	BQ158923	BQ158923 NF083A12P
c 23	607.8	7.1	795	5	BQ157846	BQ157846 NF098C12P
c 24	607.8	7.1	799	1	AV405326	AV405326 AV405326
c 25	607.8	7.1	810	7	CV478551	CV478551 Lu6B6 Fla
c 26	607.8	7.1	815	7	CV478075	CV478075 Lu1A6 Fla
c 27	606.8	7.1	757	5	BQ158987	BQ158987 NF100G10P
c 28	606.8	7.1	758	5	BQ159010	BQ159010 NF102E04P
c 29	606.8	7.1	762	5	BQ158850	BQ158850 NF073H10P
c 30	606.8	7.1	768	5	BQ158329	BQ158329 NF047G06P
c 31	606.8	7.1	769	5	BQ159407	BQ159407 NF120B04P
c 32	606.8	7.1	770	5	BQ158852	BQ158852 NF074B11P
c 33	606.8	7.1	771	5	BQ158940	BQ158940 NF095A10P
c 34	606.8	7.1	776	5	BQ158753	BQ158753 NF071A06P
c 35	606.8	7.1	777	5	BQ159021	BQ159021 NF103G05P
c 36	606.8	7.1	779	5	BQ159399	BQ159399 NF118A11P
c 37	606.8	7.1	781	5	BQ158877	BQ158877 NF076G10P
c 38	606.8	7.1	781	5	BQ159263	BQ159263 NF090H06P
c 39	606.8	7.1	782	5	BQ158858	BQ158858 NF075C06P
c 40	606.8	7.1	784	5	BQ158848	BQ158848 NF074A07P
c 41	606.8	7.1	784	5	BQ158973	BQ158973 NF098A03P
c 42	606.8	7.1	786	5	BQ159035	BQ159035 NF104H08P
c 43	606.8	7.1	788	5	BQ158195	BQ158195 NF031B09P
c 44	606.8	7.1	792	5	BQ158756	BQ158756 NF071E09P
c 45	606.8	7.1	799	5	BQ158971	BQ158971 NF097D10P

ALIGNMENTS

RESULT 1
CN385673/c
LOCUS CN385673 813 bp mRNA linear EST 31-AUG-2004
DEFINITION LE2TR04D22 Tomato CL5915 roots under different developmental stages
Lycopersicon esculentum cDNA clone LE2TR04D22, mRNA sequence.
ACCESSION CN385673
VERSION CN385673.1 GI:51700987
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 813)
AUTHORS Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
TITLE DNA microarray profiling of gene expression during tomato root development
JOURNAL Unpublished (2004)
COMMENT Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of BioAgricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2561-5600
Email: kyto@gate.sinica.edu.tw
Insert Length: 813 Std Error: 0.00
Plate: 04 row: D column: 22
Seq primer: smart2.
FEATURES Location/Qualifiers
source 1. .813
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="CL5915"
/db_xref="taxon:4081"
/clone="LE2TR04D22"
/tissue_type="roots"
/dev_stage="1-,2-,3-, and 4- month-old"
/lab_host="E.coli BM25.8"
/clone_lib="Tomato CL5915 roots under different developmental stages"
/note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained from AVRDC.Roots were harvested from plants grown under different developmental stages: 1-,2-,3-,4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)"
ORIGIN

Query Match 7.2%; Score 616.8; DB 7; Length 813;
Best Local Similarity 97.4%; Pred. No. 1.5e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 2
CV089193/c

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LOCUS       CV089193                860 bp    mRNA    linear   EST 26-AUG-2004
DEFINITION  est_c_virginica2856 Cv Hepatopancreas Crassostrea virginica cDNA,
            mRNA sequence.
ACCESSION   CV089193
VERSION     CV089193.1  GI:51568542
KEYWORDS    EST.
SOURCE      Crassostrea virginica (eastern oyster)
  ORGANISM  Crassostrea virginica
            Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida;
            Ostreoidea; Ostreidae; Crassostrea.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   Jenny,M.J., Warr,G.W., Gross,P.S., Almeida,J.S., Chen,Y.,
            McKillen,D.J., Wu,S. and Chapman,R.W.
  TITLE     Crassostrea virginica EST Library at marinegenomics.org
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Gross PS
            Department of Biochemistry and Molecular Biology
            Medical University of South Carolina
            Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA
            Tel: 846 792 8503
            Fax: 843 792 4850
            Email: grossp@musc.edu.
FEATURES             Location/Qualifiers
     source          1. .860
                     /organism="Crassostrea virginica"
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                     /db_xref="taxon:6565"
                     /cell_type="hepatopancreas"
                     /clone_lib="Cv Hepatopancreas"
                     /note="Vector: pTriplEx2; Site_1: Sfi I; Site_2: Sfi I"
ORIGIN
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Query Match 7.2%; Score 616.8; DB 7; Length 860;
Best Local Similarity 97.4%; Pred. No. 1.6e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 648

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 588

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 528

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 468

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 408

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 348

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 288

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
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Db        107 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 64
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RESULT 3
CN385663/c

```
LOCUS       CN385663                862 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  LE2TR04D12 Tomato CL5915 roots under different developmental stages
            Lycopersicon esculentum cDNA clone LE2TR04D12, mRNA sequence.
ACCESSION   CN385663
VERSION     CN385663.1  GI:51700977
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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REFERENCE   1  (bases 1 to 862)
  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
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            Plate: 04  row: D  column: 12
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FEATURES             Location/Qualifiers
     source          1. .862
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                     /db_xref="taxon:4081"
                     /clone="LE2TR04D12"
                     /tissue_type="roots"
                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN

  Query Match             7.2%;  Score 616.8;  DB 7;  Length 862;
  Best Local Similarity   97.4%;  Pred. No. 1.6e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
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Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
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Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||      |    || | |  ||  | |||
Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 4
CN385637/c
LOCUS       CN385637                874 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  LE2TR04C09 Tomato CL5915 roots under different developmental stages
            Lycopersicon esculentum cDNA clone LE2TR04C09, mRNA sequence.
ACCESSION   CN385637
VERSION     CN385637.1  GI:51700951
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
            Insert Length: 874   Std Error: 0.00
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            Seq primer: smart2.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:4081"
                     /clone="LE2TR04C09"
                     /tissue_type="roots"
                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN

  Query Match             7.2%;  Score 616.8;  DB 7;  Length 874;
  Best Local Similarity   97.4%;  Pred. No. 1.6e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
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Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
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Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
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Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
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Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
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Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||||      |    || | |  ||  | |||
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RESULT 5
CN385877/c

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LOCUS       CN385877                884 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  LE2TR04M16 Tomato CL5915 roots under different developmental stages
            Lycopersicon esculentum cDNA clone LE2TR04M16, mRNA sequence.
ACCESSION   CN385877
VERSION     CN385877.1  GI:51701191
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
            Insert Length: 884    Std Error: 0.00
            Plate: 04  row: M  column: 16
            Seq primer: smart2.
FEATURES             Location/Qualifiers
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                     /clone="LE2TR04M16"
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                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN
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Query Match 7.2%; Score 616.8; DB 7; Length 884;
Best Local Similarity 97.4%; Pred. No. 1.6e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
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Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
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Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
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Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
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Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||||      |    || | |  ||  | |||
Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 6
CN385574/c

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LOCUS       CN385574                899 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  LE2TR03P18 Tomato CL5915 roots under different developmental stages
            Lycopersicon esculentum cDNA clone LE2TR03P18, mRNA sequence.
ACCESSION   CN385574
VERSION     CN385574.1  GI:51700888
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 899)
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  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
            Insert Length: 899   Std Error: 0.00
            Plate: 03  row: P  column: 18
            Seq primer: smart2.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="CL5915"
                     /db_xref="taxon:4081"
                     /clone="LE2TR03P18"
                     /tissue_type="roots"
                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN

  Query Match           7.2%;  Score 616.8;  DB 7;  Length 899;
  Best Local Similarity  97.4%;  Pred. No. 1.6e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
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Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520

Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
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Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
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Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
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Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
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Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56


RESULT 7
CN384456/c
LOCUS       CN384456                 921 bp    mRNA    linear   EST 31-AUG-2004
DEFINITION  LE2TR01A01 Tomato CL5915 roots under different developmental stages
            Lycopersicon esculentum cDNA clone LE2TR01A01, mRNA sequence.
ACCESSION   CN384456
VERSION     CN384456.1  GI:51699770
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
  TITLE     DNA microarray profiling of gene expression during tomato root
            development
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Kin-Ying, To
            Crop Plant Improvement Group
            Institute of BioAgricultural Sciences, Academia Sinica
            128 Academia Rd. Section 2, Taipei, Taiwan 11529
            Tel: 886-2-2653-3161
            Fax: 886-2-2561-5600
            Email: kyto@gate.sinica.edu.tw
            Insert Length: 921   Std Error: 0.00
            Plate: 01  row: A  column: 01
            Seq primer: smart2.
FEATURES             Location/Qualifiers
     source          1. .921
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                     /mol_type="mRNA"
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                     /db_xref="taxon:4081"
                     /clone="LE2TR01A01"
                     /tissue_type="roots"
                     /dev_stage="1-,2-,3-, and 4- month-old"
                     /lab_host="E.coli BM25.8"
                     /clone_lib="Tomato CL5915 roots under different
                     developmental stages"
                     /note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
                     from AVRDC.Roots were harvested from plants grown under
                     different developmental stages: 1-,2-,3-,4-month-old.
                     Equal aliquots of mRNA of different developmental stages
                     were mixed and used for cDNA library construction. (Smart
                     PCR cDNA Library construction kit, Clontech)"
ORIGIN

  Query Match           7.2%;  Score 616.8;  DB 7;  Length 921;
  Best Local Similarity  97.4%;  Pred. No. 1.6e-174;
  Matches  627;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 GACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC 640

Qy         63 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCC 580

Qy        123 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 ACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 520
```

```
Qy        183 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 AGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGG 460

Qy        243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT 400

Qy        303 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 GGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTA 340

Qy        363 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 TAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTT 280

Qy        423 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 AACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCGCA 220

Qy        483 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

Qy        543 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 GATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTA 100

Qy        603 AAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              ||||||||||||||||    |  || | |  ||  | |||
Db         99 AAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 8
BE421195/c

```
LOCUS       BE421195                 805 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  HWM006.G08 ITEC HWM Barley Leaf Library Hordeum vulgare subsp.
            vulgare cDNA clone HWM006.G08, mRNA sequence.
ACCESSION   BE421195
VERSION     BE421195.1  GI:9419038
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 805)
  AUTHORS   Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,
            Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,
            Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,
            Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,
            Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,
            Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
  TITLE     International Triticeae EST Cooperative (ITEC): Production of
            Expressed Sequence Tags for Species of the Triticeae
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Herrmann RG
            Botanisches Institut der LMU
            Menzinger Str. 67, D-80638 Munchen GERMANY
            Fax: 49 30 171683
            Email: herrmann@botanik.biologie.uni-muenchen.de
            International Triticeae EST Cooperative (ITEC)
            http://wheat.pw.usda.gov/genome.
FEATURES             Location/Qualifiers
     source          1. .805
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="barke"
                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="HWM006.G08"
                     /tissue_type="leaf"
                     /dev_stage="14 day old"
                     /clone_lib="ITEC HWM Barley Leaf Library"
                     /note="Vector: pBluescriptSK(-); 850 bp average insert
                     size."
ORIGIN
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  Query Match             7.1%;  Score 608.8;  DB 2;  Length 805;
  Best Local Similarity   99.4%;  Pred. No. 4.1e-172;
  Matches  621;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              |||||||| |||||||||||||||||||| || ||||||||||||||||||||||||||||
Db        777 CTGACGCGGCCTGTAGCGGCGCATTAAGCNCGCCGGGTGTGGTGGTTACGCGCAGCGTGA 718

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 658

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 598

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 538

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 478

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 418

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTT-AAAAAATGAGCTGATTTAACAAAAA 419
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        417 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAAATGAGCTGATTTAACAAAAA 358

Qy        420 TTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGC 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 TTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGC 298

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 238

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 178

Qy        600 GTAAAACGACGGCCAGTGAGCGCGC 624
              |||||||||||||||||||||||||
Db        177 GTAAAACGACGGCCAGTGAGCGCGC 153
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RESULT 9
BU724260/c

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LOCUS       BU724260                 685 bp    mRNA    linear   EST 23-OCT-2003
DEFINITION  SJMBFC05 SJM Schistosoma japonicum cDNA similar to gb|AAB53629.1|
            (U84006) beta-galactosidase [Expression vector pBSII-LUCINT], mRNA
            sequence.
ACCESSION   BU724260
VERSION     BU724260.1  GI:28331629
KEYWORDS    EST.
SOURCE      Schistosoma japonicum
  ORGANISM  Schistosoma japonicum
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 685)
  AUTHORS   Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
            Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
            Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
            McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
```

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  TITLE     Evolutionary and biomedical implications of a Schistosoma japonicum
            complementary DNA resource
  JOURNAL   Nat. Genet. 35 (2), 139-147 (2003)
  MEDLINE   22879925
   PUBMED   12973349
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn.
FEATURES             Location/Qualifiers
     source          1. .685
                     /organism="Schistosoma japonicum"
                     /mol_type="mRNA"
                     /db_xref="taxon:6182"
                     /sex="male"
                     /tissue_type="Whole body"
                     /dev_stage="adult"
                     /lab_host="rabbits"
                     /clone_lib="SJM"
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 5;  Length 685;
  Best Local Similarity   97.2%;  Pred. No. 7.8e-172;
  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        675 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 616

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 556

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 496

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 436

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 376

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 316

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 256

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        255 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 196

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 136

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 76

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db         75 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 29
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RESULT 10
CB549906/c
LOCUS       CB549906                 702 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  MMPL0007_B01 MMPL Macaca mulatta cDNA, mRNA sequence.
ACCESSION   CB549906
VERSION     CB549906.1  GI:31299101
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 702)
  AUTHORS   Katze,M.G., Bumgarner,R., Korth,M., Feldman,R., Amjadi,M. and
            Holzman,T.
  TITLE     Expressed sequence tags from Rhesus macaque placenta
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Holzman T
            Katze Lab
            University of Washington
            Box 358070, Seattle, WA 98195-8070, USA
            Tel: 206 732 6156
            Fax: 206 732 6055
            Email: ted@locke.hs.washington.edu
            Similar to GenBank entry HSU94592 U94592 Human uncoupling protein
            homolog (UCPH) mRNA, complete cds. 6/2002
            Plate: MMPL0007  row: B  column: 01.
FEATURES             Location/Qualifiers
     source          1. .702
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /sex="male"
                     /dev_stage="neonatal"
                     /clone_lib="MMPL"
                     /note="Organ: placenta"
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 6;  Length 702;
  Best Local Similarity   97.2%;  Pred. No. 7.9e-172;
  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 610

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 550

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 490

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 430

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 370

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 310

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 250

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        249 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 190
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Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 130

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 70

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db         69 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 23
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RESULT 11
CB548528/c

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LOCUS       CB548528                714 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  MMPL0022_H09 MMPL Macaca mulatta cDNA, mRNA sequence.
ACCESSION   CB548528
VERSION     CB548528.1  GI:31297723
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 714)
  AUTHORS   Katze,M.G., Bumgarner,R., Korth,M., Feldman,R., Amjadi,M. and
            Holzman,T.
  TITLE     Expressed sequence tags from Rhesus macaque placenta
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Holzman T
            Katze Lab
            University of Washington
            Box 358070, Seattle, WA 98195-8070, USA
            Tel: 206 732 6156
            Fax: 206 732 6055
            Email: ted@locke.hs.washington.edu
            Similar to GenBank entry HSU94592 U94592 Human uncoupling protein
            homolog (UCPH) mRNA, complete cds. 6/2002
            Plate: MMPL0022  row: H  column: 09.
FEATURES             Location/Qualifiers
     source          1. .714
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /sex="male"
                     /dev_stage="neonatal"
                     /clone_lib="MMPL"
                     /note="Organ: placenta"
ORIGIN
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Query Match 7.1%; Score 607.8; DB 6; Length 714;
Best Local Similarity 97.2%; Pred. No. 7.9e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

```
Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 643

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 583

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 523

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 463

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 403

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 343

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 283

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        282 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 223

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 163

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 103

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||||||       |    || | |  ||  | |||
Db        102 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 12
BQ157858/c

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LOCUS       BQ157858                753 bp    mRNA    linear   EST 24-APR-2002
DEFINITION  NF103A09PL1F1067 Phosphate starved leaf Medicago truncatula cDNA
            clone NF103A09PL 5', mRNA sequence.
ACCESSION   BQ157858
VERSION     BQ157858.1  GI:20294915
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Insert Length: 753  Std Error: 0.00
            Plate: 103  row: A  column: 09
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .753
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                     /mol_type="mRNA"
                     /db_xref="taxon:3880"
                     /clone="NF103A09PL"
                     /tissue_type="leaf"
                     /dev_stage="trifoliate"
                     /clone_lib="Phosphate starved leaf"
                     /note="Vector: Lambda Zap; At the trifoliate stage, M.
                     truncatula plants were transplanted to phosphate-free sand
                     and grown for a further 30 days.  During this 30 day
                     period, the plants were fertilized twice weekly with 1/2
                     Hoaglands solution containing only 20uM potassium
                     phosphate.  RNA was prepared from above ground tissues."
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ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 5;  Length 753;
  Best Local Similarity   97.2%;  Pred. No. 8.1e-172;
  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 689

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 629

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 569

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 509

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 449

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 389

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 329

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
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Db        328 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 269

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 209

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 149

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||||||      |    || | |  || | |||
Db        148 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 102


RESULT 13
BQ158943/c
LOCUS       BQ158943                758 bp    mRNA    linear   EST 24-APR-2002
DEFINITION  NF095D07PL1F1060 Phosphate starved leaf Medicago truncatula cDNA
            clone NF095D07PL 5', mRNA sequence.
ACCESSION   BQ158943
VERSION     BQ158943.1  GI:20296000
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 758)
  AUTHORS   Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Insert Length: 758   Std Error: 0.00
            Plate: 095  row: D  column: 07
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .758
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                     /mol_type="mRNA"
                     /db_xref="taxon:3880"
                     /clone="NF095D07PL"
                     /tissue_type="leaf"
                     /dev_stage="trifoliate"
                     /clone_lib="Phosphate starved leaf"
                     /note="Vector: Lambda Zap; At the trifoliate stage, M.
                     truncatula plants were transplanted to phosphate-free sand
                     and grown for a further 30 days.  During this 30 day
                     period, the plants were fertilized twice weekly with 1/2
                     Hoaglands solution containing only 20uM potassium
                     phosphate.  RNA was prepared from above ground tissues."
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 5;  Length 758;
  Best Local Similarity   97.2%;  Pred. No. 8.1e-172;
  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 688

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 628

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 568

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 508

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 448

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 388

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 328

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        327 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 268

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 208

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 148

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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Db        147 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 101
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RESULT 14
BQ158750/c
LOCUS       BQ158750                764 bp    mRNA    linear   EST 24-APR-2002
DEFINITION  NF070F07PL1F1061 Phosphate starved leaf Medicago truncatula cDNA
            clone NF070F07PL 5', mRNA sequence.
ACCESSION   BQ158750
VERSION     BQ158750.1  GI:20295807
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 764)
  AUTHORS   Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Insert Length: 764    Std Error: 0.00
            Plate: 070  row: F  column: 07
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
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                     /clone_lib="Phosphate starved leaf"
                     /note="Vector: Lambda Zap; At the trifoliate stage, M.
                     truncatula plants were transplanted to phosphate-free sand
                     and grown for a further 30 days.  During this 30 day
                     period, the plants were fertilized twice weekly with 1/2
                     Hoaglands solution containing only 20uM potassium
                     phosphate.  RNA was prepared from above ground tissues."
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 5;  Length 764;
  Best Local Similarity   97.2%;  Pred. No. 8.1e-172;
  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 689

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 629

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 569

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 509

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 449

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 389

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 329

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        328 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 269

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
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Db        268 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 209

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 149

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
              |||||||||||||||||||  |  ||| | |  || | |||
Db        148 GTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAA 102


RESULT 15
BQ158875/c
LOCUS       BQ158875                771 bp    mRNA    linear   EST 24-APR-2002
DEFINITION  NF076G06PL1F1050 Phosphate starved leaf Medicago truncatula cDNA
            clone NF076G06PL 5', mRNA sequence.
ACCESSION   BQ158875
VERSION     BQ158875.1  GI:20295932
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Insert Length: 771    Std Error: 0.00
            Plate: 076  row: G  column: 06
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:3880"
                     /clone="NF076G06PL"
                     /tissue_type="leaf"
                     /dev_stage="trifoliate"
                     /clone_lib="Phosphate starved leaf"
                     /note="Vector: Lambda Zap; At the trifoliate stage, M.
                     truncatula plants were transplanted to phosphate-free sand
                     and grown for a further 30 days.  During this 30 day
                     period, the plants were fertilized twice weekly with 1/2
                     Hoaglands solution containing only 20uM potassium
                     phosphate.  RNA was prepared from above ground tissues."
ORIGIN

  Query Match             7.1%;  Score 607.8;  DB 5;  Length 771;
  Best Local Similarity   97.2%;  Pred. No. 8.2e-172;
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  Matches  629;  Conservative    0;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 691

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 631

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 571

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 511

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 451

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 391

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 331

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTT-CCATTCGCCATTCAGGCTGC 479
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        330 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTGCCATTCGCCATTCAGGCTGC 271

Qy        480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG 211

Qy        540 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 599
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Db        210 GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT 151

Qy        600 GTAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAA 646
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 2688 Seconds
(without alignments)
18805.309 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8539	100.0	11282	2	AAZ27850	Aaz27850 Complete
2	8539	100.0	11282	4	AAD04741	Aad04741 Alphavira
3	8539	100.0	11282	5	AAF84024	Aaf84024 Complete
4	8539	100.0	11282	12	ADL71889	Adl71889 Temperatu
5	7657.2	89.7	13068	12	ADL71890	Adl71890 Temperatu
6	7657.2	89.7	15081	12	ADL71909	Adl71909 Expressio
7	7657.2	89.7	17753	12	ADL71910	Adl71910 Expressio
8	7637.4	89.4	9951	2	AAX77354	Aax77354 Polynucle
9	7637.4	89.4	9951	3	AAA90386	Aaa90386 Sindbis e
10	7637.4	89.4	9951	4	AAD04742	Aad04742 Alphavira
11	7637.4	89.4	9951	6	ABN86686	Abn86686 Nucleotid
12	7637.4	89.4	9951	6	ABV73174	Abv73174 Nucleotid
13	7637.4	89.4	12110	6	ABN86689	Abn86689 Nucleotid
14	7637.4	89.4	13905	2	AAX77358	Aax77358 Polynucle
15	7637.4	89.4	13905	3	AAA90390	Aaa90390 Plasmid p
16	7635.8	89.4	10524	2	AAX77355	Aax77355 Polynucle
17	7635.8	89.4	10524	3	AAA90387	Aaa90387 Plasmid p
18	7634.8	89.4	8000	8	ABX81525	Abx81525 Sindbis v
19	7634.8	89.4	8000	9	ADA50625	Ada50625 SINCG vir
20	7634.8	89.4	11703	13	ADR32077	Adr32077 Genomic D
21	7634.8	89.4	11703	13	ADR67767	Adr67767 Sindbis v
22	7634.8	89.4	11740	8	ABX81526	Abx81526 Sindbis v
23	7634.8	89.4	11740	9	ADA50626	Ada50626 Toto 1101
24	7634.2	89.4	16847	12	ADO07464	Ado07464 Japanese
25	7632.6	89.4	11927	2	AAX77356	Aax77356 Polynucle
26	7632.6	89.4	11927	3	AAA90388	Aaa90388 Plasmid p
27	7623.6	89.3	11703	3	AAC64506	Aac64506 Alphaviru
28	7620.4	89.2	11703	3	AAC64507	Aac64507 Alphaviru
29	7618.8	89.2	11703	2	AAV33476	Aav33476 Sindbis v
30	7617.2	89.2	8000	2	AAX59321	Aax59321 Sindbis v
31	7617.2	89.2	8000	2	AAX58571	Aax58571 Sindbis v
32	7617.2	89.2	8000	8	ABX81524	Abx81524 Sindbis v
33	7617.2	89.2	8000	9	ADA50624	Ada50624 SIN-1 vir
34	7612.4	89.1	16656	2	AAQ86154	Aaq86154 Eukaryoti
35	7612.4	89.1	16656	2	AAV42364	Aav42364 Represent
36	7612.4	89.1	16656	2	AAV60125	Aav60125 Represent
37	7612.4	89.1	16656	2	AAV70684	Aav70684 Represent
38	7612.4	89.1	16656	3	AAZ92892	Aaz92892 Represent
39	7612.4	89.1	16656	3	AAZ92765	Aaz92765 Represent
40	7612.4	89.1	16656	6	AAL38772	Aal38772 DNA of eu
41	7612.4	89.1	16656	12	ADI30344	Adi30344 Eukaryoti
42	7610.8	89.1	16656	6	ABK46238	Abk46238 Eukaryoti
43	7602.8	89.0	16656	2	AAT30787	Aat30787 Alphaviru
44	7598.8	89.0	16958	8	AAL55269	Aal55269 DNA of ex
45	7457	87.3	11687	6	AAD25136	Aad25136 SinChiron

ALIGNMENTS

RESULT 1
AAZ27850
ID AAZ27850 standard; cDNA; 11282 BP.
XX
AC AAZ27850;
XX
DT 23-DEC-1999 (first entry)
XX
DE Complete cDNA sequence of pCYTts.
XX
KW Gene expression system; cis-acting element; gene therapy;
KW temperature-sensitive RNA-dependent RNA polymerase;
KW inducible alphaviral gene expression system; pCYTts;
KW hormone-based gene control system; tetracycline gene control system; ss.
XX
OS Synthetic.
XX
PN WO9950432-A1.
XX
PD 07-OCT-1999.
XX
PF 25-MAR-1999; 99WO-IB000523.
XX
PR 27-MAR-1998; 98US-0079562P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (RENN/) RENNER W A.
PA (NIEB/) NIEBA L.
PA (BOOR/) BOORSMA M.
XX
PI Renner WA, Nieba L, Boorsma M;
XX
DR WPI; 1999-591327/50.
XX
PT A new system to regulate gene expression in eukaryotic cells.
XX
PS Claim 15; Fig 3; 99pp; English.
XX
CC This sequence represents the complete cDNA sequence for the vector
CC pCYTts. The invention relates to a DNA molecule comprising a
CC polynucleotide (I) encoding an RNA molecule. The encoded RNA comprises:
CC (a) at least one cis-acting element; (b) an open reading frame (ORF1)
CC encoding a non-cytopathic, temperature-sensitive RNA-dependent RNA

CC polymerase; and (c) a second sequence that is: (i) a protein-encoding ORF
CC (ORF2) that is in a translatable format after RNA-dependent RNA
CC replication event(s); (ii) a sequence complementary to the ORF2; or (iii)
CC a sequence encoding an untranslated RNA molecule. The pCYTts sequence is
CC an example of the DNA molecule, and is an inducible alphaviral gene
CC expression system. The invention is used in gene therapy and recombinant
CC technology to regulate expression of introduced genes. The invention does
CC not have the problems of toxicity and/or high basal level expression
CC associated with prior art tetracycline-based and hormone-based gene
CC control systems
XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 2; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480

Qy        481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540

Qy        541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600

Qy        601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660

Qy        661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720

Qy        721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780

Qy        781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840

Qy        841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900

Qy        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960

Qy        961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020

Qy       1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080

Qy       1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140

Qy       1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200

Qy       1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260

Qy       1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320

Qy       1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380

Qy       1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440

Qy       1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500

Qy       1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560

Qy       1561 AAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAGGTAGGACA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAGGTAGGACA 1620

Qy       1621 GGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTTATTTCTCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTTATTTCTCC 1680

Qy       1681 GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATCTTCCATCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATCTTCCATCG 1740

Qy       1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800

Qy       1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860

Qy       1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920

Qy       1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980
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Db      1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980
Qy      1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040
Db      1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040
Qy      2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
Db      2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
Qy      2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
Db      2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
Qy      2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
Db      2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
Qy      2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280
Db      2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280
Qy      2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
Db      2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
Qy      2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
Db      2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
Qy      2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
Db      2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
Qy      2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
Db      2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
Qy      2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
Db      2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
Qy      2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
Db      2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
Qy      2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
Db      2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
Qy      2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
Db      2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
Qy      2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
Db      2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
Qy      2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
Db      2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
Qy      2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
Db      2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
Qy      2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
Db      2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
Qy      3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
Db      3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
Qy      3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
Db      3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
Qy      3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Db      3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Qy      3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Db      3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Qy      3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
Db      3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
Qy      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Db      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Qy      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Db      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Qy      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Db      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Qy      3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Db      3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Qy      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Db      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Qy      3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Db      3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Qy      3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
Db      3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
Qy      3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
Db      3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
Qy      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Db      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Qy      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Db      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Qy      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Db      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Qy      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Db      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Qy      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Db      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Qy      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
Db      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
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Qy      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200

Qy      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260

Qy      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320

Qy      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380

Qy      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440

Qy      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500

Qy      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560

Qy      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620

Qy      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680

Qy      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740

Qy      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800

Qy      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860

Qy      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920

Qy      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980

Qy      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040

Qy      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100

Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160

Qy      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220

Qy      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280

Qy      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340

Qy      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400

Qy      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460

Qy      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520

Qy      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580

Qy      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640

Qy      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700

Qy      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760

Qy      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820

Qy      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880

Qy      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940

Qy      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000

Qy      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060

Qy      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120

Qy      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180

Qy      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240

Qy      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300

Qy      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
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Db      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
Qy      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
Db      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
Qy      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
Db      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
Qy      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
Db      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
Qy      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
Db      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
Qy      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
Db      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
Qy      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
Db      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
Qy      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
Db      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
Qy      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
Db      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
Qy      6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
Db      6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
Qy      6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Db      6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Qy      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Db      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Qy      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Db      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Qy      7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
Db      7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
Qy      7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
Db      7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
Qy      7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
Db      7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
Qy      7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
Db      7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
Qy      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Db      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Qy      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Db      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Qy      7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
Db      7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
Qy      7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
Db      7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
Qy      7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
Db      7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
Qy      7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Db      7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Qy      7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Db      7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Qy      7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Db      7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Qy      7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
Db      7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
Qy      7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
Db      7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
Qy      7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
Db      7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
Qy      7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
Db      7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
Qy      8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Db      8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Qy      8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
Db      8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
Qy      8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
Db      8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
Qy      8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
Db      8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
Qy      8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
Db      8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
Qy      8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
Db      8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
Qy      8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
Db      8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
Qy      8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
Db      8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
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Qy       8521 TACTACAACACCACCACCT 8539
             ||||||||||||||||||||
Db       8521 TACTACAACACCACCACCT 8539
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RESULT 2
AAD04741
ID AAD04741 standard; cDNA; 11282 BP.
XX
AC AAD04741;
XX
DT 17-JUL-2001 (first entry)
XX
DE Alphaviral vector pCYTts cDNA.
XX
KW pCYTts; alphaviral vector; vaccine; therapy; cancer; antiparasitic;
KW antimalarial; anticancer; anti-HIV; antiviral; infectious disease;
KW Human immunodeficiency virus; HIV; influenza; passive immunisation;
KW carcinoma; liver; skin; stomach; ovarian tumour; ss.
XX
OS Rous sarcoma virus.
OS Alphavirus.
OS Unidentified.
OS Chimeric.
XX
PN WO200130989-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-IB001557.
XX
PR 27-OCT-1999; 99US-0161796P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (RENN/) RENNER W A.
PA (NIEB/) NIEBA L.
XX
PI Renner WA, Nieba L;
XX
DR WPI; 2001-308631/32.
XX
PT Preparing alphaviral vectors with mutations in a selected gene, for use
PT as vaccines, particularly against pathogens that mutate rapidly,
PT comprises replicating in the presence of a nucleoside analog.
XX
PS Claim 6; Fig 3; 103pp; English.
XX
CC The present invention relates to a method for preparing viral vectors
CC which comprises inserting a gene of interest into an alphaviral vector
CC such as pCYTts, pSinRep5 and replicating the vector in the presence of
CC alphaviral replicase and nucleoside analogues (5'azacytidine (AZT), FU-
CC 5' fluorouridine) to produce a modified gene of interest. The replication
CC is repeated until the modified gene in 90 % of the vector population
CC contain a mutation in the modified gene which is 90-99 % identical with
CC the gene of interest. The vector populations are used in vaccines for
CC treatment or prevention of a wide variety of infectious diseases (viral
CC or parasitic, e.g. human immuno deficiency virus (HIV), influenza,
CC Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach
CC carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the
CC mutant populations will therefore be effective against viral escape
CC mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins
CC are correctly glycosylated. Antisera raised against the vaccines can be
CC used for passive immunisation. The present cDNA sequence is an alphaviral
CC vector pCYTts. The vector contains Rous Sarcoma Virus promoter, cis-
CC acting sequence elements, non-structural proteins 1-4, gene of interest,
CC alphavirus subgenomic promoter, ampicillin resistance marker for
CC selection and a CoIE1 sequence for bacterial amplification
XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 4; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480

Qy        481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540

Qy        541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600

Qy        601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660

Qy        661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720

Qy        721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780

Qy        781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840

Qy        841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900

Qy        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960

Qy        961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020

Qy       1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
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Qy       1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140

Qy       1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200

Qy       1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260

Qy       1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320

Qy       1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380

Qy       1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440

Qy       1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500

Qy       1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560

Qy       1561 AAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAGGTAGGACA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAGGTAGGACA 1620

Qy       1621 GGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTTATTTCTCC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTTATTTCTCC 1680

Qy       1681 GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATCTTCCATCG 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATCTTCCATCG 1740

Qy       1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800

Qy       1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860

Qy       1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920

Qy       1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980

Qy       1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040

Qy       2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100

Qy       2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160

Qy       2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220

Qy       2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280

Qy       2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340

Qy       2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400

Qy       2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460

Qy       2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520

Qy       2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580

Qy       2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640

Qy       2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700

Qy       2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760

Qy       2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820

Qy       2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880

Qy       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940

Qy       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000

Qy       3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060

Qy       3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120

Qy       3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180

Qy       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240

Qy       3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
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Db      3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
Qy      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Db      3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Qy      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Db      3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Qy      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Db      3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Qy      3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Db      3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Qy      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Db      3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Qy      3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Db      3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Qy      3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
Db      3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
Qy      3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
Db      3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
Qy      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Db      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Qy      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Db      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Qy      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Db      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Qy      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Db      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Qy      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Db      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Qy      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
Db      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
Qy      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
Db      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
Qy      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
Db      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
Qy      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
Db      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
Qy      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
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Db      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
Qy      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
Db      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
Qy      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
Db      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
Qy      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
Db      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
Qy      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
Db      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
Qy      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
Db      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
Qy      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
Db      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
Qy      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
Db      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
Qy      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
Db      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
Qy      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
Db      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
Qy      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
Qy      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
Db      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
Qy      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
Db      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
Db      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
Qy      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
Db      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
Qy      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
Db      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
Qy      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
Db      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
Qy      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
Db      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
Qy      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
Db      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
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Qy      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520

Qy      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580

Qy      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640

Qy      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700

Qy      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760

Qy      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820

Qy      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880

Qy      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940

Qy      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000

Qy      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060

Qy      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120

Qy      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180

Qy      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240

Qy      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300

Qy      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360

Qy      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420

Qy      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480

Qy      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540

Qy      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600

Qy      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660

Qy      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720

Qy      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780

Qy      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840

Qy      6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900

Qy      6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960

Qy      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020

Qy      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080

Qy      7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140

Qy      7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200

Qy      7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260

Qy      7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320

Qy      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380

Qy      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440

Qy      7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500

Qy      7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560

Qy      7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620

Qy      7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
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Db       7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680

Qy       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740

Qy       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800

Qy       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860

Qy       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920

Qy       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980

Qy       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040

Qy       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100

Qy       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160

Qy       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220

Qy       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280

Qy       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340

Qy       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400

Qy       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460

Qy       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520

Qy       8521 TACTACAACACCACCACCT 8539
             ||||||||||||||||||||
Db       8521 TACTACAACACCACCACCT 8539
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RESULT 3
AAF84024
ID AAF84024 standard; cDNA; 11282 BP.
XX
AC AAF84024;
XX
DT 22-AUG-2001 (first entry)
XX
DE Complete cDNA sequence of plasmid pCYTt.
XX
KW pCYTt; cellular; taxol; gene therapy; RNA replication; endogenous gene;
KW ss.
XX
OS Synthetic.
XX
PN WO200142442-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-IB001841.
XX
PR 10-DEC-1999; 99US-0169988P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Hennecke F, Renner WA;
XX
DR WPI; 2001-381672/40.
XX
PT Modifying endogenous target gene expression in eukaryotic cell for
PT performing gene therapy, involves inserting exogenous polynucleotides in
PT gene to produce recombinant eukaryotic host cell and culturing the cell.
XX
PS Disclosure; Fig 8A-D; 131pp; English.
XX
CC The invention relates to a method of modifying expression characteristics
CC of an endogenous target gene within a genome of a eukaryotic cell or
CC producing a polypeptide encoded by the target gene of a eukaryotic cell.
CC The method involves inserting exogenous polynucleotides in 5' and 3'
CC regions flanking the coding region of target gene to produce a
CC recombinant eukaryotic host cell, and culturing the cell. The method is
CC useful for producing cells which exhibit increased expression of
CC endogenous genes which lead to the production of additional products, and
CC for amplifying endogenous genes involved in the production of cellular
CC products such as taxol. The method is also useful for producing
CC biological products, and their derivatives, and for regulating the
CC activity of target genes by modifying the expression of regulatory
CC proteins involved in the regulation of the target genes. The method or a
CC DNA vector system is useful for performing gene therapy on an individual
CC (e.g., domesticated animal or human). The present sequence represents the
CC complete cDNA sequence of a vector pCYTts, a DNA vector system for
CC modifying the expression characteristics of an endogenous target gene
CC within the genome of a eukaryotic cell comprising a 5' targeting
CC construct and a 3' targeting construct, where the 5' and 3' targeting
CC construct encode genetic elements required for RNA replication
XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 5; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA 60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
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Qy      301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
Db      301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360

Qy      361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
Db      361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420

Qy      421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480
Db      421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480

Qy      481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540
Db      481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540

Qy      541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600
Db      541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600

Qy      601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660
Db      601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660

Qy      661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720
Db      661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720

Qy      721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780
Db      721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780

Qy      781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840
Db      781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840

Qy      841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900
Db      841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900

Qy      901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960
Db      901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960

Qy      961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
Db      961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020

Qy     1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
Db     1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080

Qy     1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140
Db     1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140

Qy     1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
Db     1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200

Qy     1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260
Db     1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260

Qy     1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320
Db     1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320

Qy     1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380
Db     1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380

Qy     1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440
Db     1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440

Qy     1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500
Db     1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500

Qy     1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560
Db     1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560

Qy     1561 AAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAGGTAGGACA 1620
Db     1561 AAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAGGTAGGACA 1620

Qy     1621 GGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTTATTTCTCC 1680
Db     1621 GGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTTATTTCTCC 1680

Qy     1681 GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATCTTCCATCG 1740
Db     1681 GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATCTTCCATCG 1740

Qy     1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800
Db     1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800

Qy     1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860
Db     1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860

Qy     1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920
Db     1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920

Qy     1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980
Db     1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980

Qy     1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040
Db     1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040

Qy     2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
Db     2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100

Qy     2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
Db     2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160

Qy     2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
Db     2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220

Qy     2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280
Db     2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280

Qy     2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
Db     2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340

Qy     2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
Db     2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400

Qy     2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
Db     2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460

Qy     2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
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Db       2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520

Qy       2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580

Qy       2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640

Qy       2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700

Qy       2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760

Qy       2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820

Qy       2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880

Qy       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940

Qy       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000

Qy       3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060

Qy       3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120

Qy       3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180

Qy       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240

Qy       3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300

Qy       3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360

Qy       3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420

Qy       3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480

Qy       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540

Qy       3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600

Qy       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660

Qy       3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720

Qy       3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780

Qy       3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840

Qy       3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900

Qy       3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960

Qy       3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020

Qy       4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080

Qy       4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140

Qy       4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200

Qy       4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260

Qy       4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320

Qy       4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380

Qy       4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440

Qy       4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500

Qy       4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560

Qy       4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620

Qy       4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
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Qy      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740

Qy      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800

Qy      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860

Qy      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920

Qy      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980

Qy      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
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Db      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040

Qy      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100

Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
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Db      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160

Qy      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220

Qy      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280

Qy      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
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Db      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340

Qy      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
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Db      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400

Qy      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
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Db      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460

Qy      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520

Qy      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580

Qy      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640

Qy      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700

Qy      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760

Qy      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820

Qy      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
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Db      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880

Qy      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
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Db      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940

Qy      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
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Db      5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000

Qy      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
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Db      6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060

Qy      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120

Qy      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180

Qy      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240

Qy      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300

Qy      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
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Db      6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360

Qy      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420

Qy      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480

Qy      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540

Qy      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600

Qy      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGGTAGGTGGG 6660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGGTAGGTGGG 6660

Qy      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720

Qy      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780

Qy      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840

Qy      6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
Qy       6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Qy       6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Qy       7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Qy       7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
Qy       7141 GCAACCTTCTGCCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GCAACCTTCTGCCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
Qy       7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
Qy       7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
Qy       7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Qy       7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Qy       7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
Qy       7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
Qy       7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
Qy       7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Qy       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Qy       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Qy       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
Qy       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
Qy       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
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Qy       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
Qy       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Qy       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
Qy       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
Qy       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
Qy       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
Qy       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
Qy       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
Qy       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
Qy       8521 TACTACAACACCACCACCT 8539
             ||||||||||||||||||||
Db       8521 TACTACAACACCACCACCT 8539
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RESULT 4
ADL71889
ID ADL71889 standard; cDNA; 11282 BP.
XX
AC ADL71889;
XX
DT 20-MAY-2004 (first entry)
XX
DE Temperature inducible alphavirus vector pCytTs.
XX
KW Gene expression; vector; pCytTS; ss.
XX
OS Rous sarcoma virus.
OS Alphavirus.
OS Chimeric.
XX
PN WO2004018506-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-EP009291.
XX
PR 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Ivanova L, Renner WA, Saudan P;
XX
DR WPI; 2004-226795/21.
XX

PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX
PS Example 1; SEQ ID NO 1; 112pp; English.
XX
CC The present sequence is that of the tightly regulated temperature
CC inducible alphavirus expression system pCytTS containing a Rous sarcoma
CC virus (RSV) promoter. The vector can be used to drive transcription of
CC mRNA from a nucleic acid molecule of the invention. A claimed nucleic
CC acid molecule comprises: (A) a first polynucleotide element which encodes
CC an RNA molecule comprising (a) at least one cis-acting sequence element,
CC (b) a first nucleotide sequence comprising a first open reading frame,
CC the first open reading frame having a nucleotide sequence encoding an RNA
CC -dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, i.e. the cis-acting replication origin oriP and the cis- or trans-
CC acting gene product EBNA-1 with pCysTS ADL71909-ADL71910. Due to the
CC presence of OriP and EBNA-1, the novel vector is maintained episomally in
CC the form of several DNA copies in cell nuclei. These multiple DNA copies
CC may be transcribed from the RSV promoter into CysTS RNA replicons, but
CC remain inactive unless cells are shifted to a certain temperature. Only
CC after temperature induction does replicon replication occur, followed by
CC RNA accumulation and translation in the cell cytoplasm, and production of
CC the polypeptide of interest.
XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 12; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA  60

Qy         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCG 120

Qy        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT 180

Qy        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTG 240

Qy        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATA 300

Qy        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATT 360

Qy        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT 420

Qy        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCATTCGCCATTCAGGCTGCG 480

Qy        481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG 540

Qy        541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTG 600

Qy        601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAAAACGACGGCCAGTGAGCGCGCAATTAACCCTCACTAAAGGGAACAAAAGCTGGCTAG 660

Qy        661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAA 720

Qy        721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CATGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTAC 780

Qy        781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAA 840

Qy        841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCGCATTGCAGAGATATTGTATTTAAGTGCCCTACCTCGATACCGTCGAGATTGACGG 900

Qy        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAATGGAGAAG 960

Qy        961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAAAAAGC 1020

Qy       1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGA 1080

Qy       1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGACGATC 1140

Qy       1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATTGTGTC 1200

Qy       1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAACTGGCG 1260

Qy       1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCCGGACC 1320

Qy       1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTACCTGC 1380

Qy       1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCGGAACTATC 1440

Qy       1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACACCACCCAG 1500

Qy       1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGGCCGACGAG 1560
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Qy       1561 AAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAGGTAGGACA 1620
Db       1561 AAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAGGTAGGACA 1620

Qy       1621 GGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTTATTTCTCC 1680
Db       1621 GGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTTATTTCTCC 1680

Qy       1681 GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATCTTCCATCG 1740
Db       1681 GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATCTTCCATCG 1740

Qy       1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800
Db       1741 GTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGGTGAGTTGC 1800

Qy       1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860
Db       1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAACCGTGGGA 1860

Qy       1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920
Db       1861 TACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACACAGTAAAA 1920

Qy       1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980
Db       1921 GGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG 1980

Qy       1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040
Db       1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGGTTGGGCTC 2040

Qy       2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100
Db       2041 AACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGCAAAATTAC 2100

Qy       2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
Db       2101 CTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGGATGATCTT 2160

Qy       2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220
Db       2161 GATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCTTGTGGGCG 2220

Qy       2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280
Db       2221 TTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCTGCGTAAAA 2280

Qy       2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340
Db       2281 GTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTTTGCCCATG 2340

Qy       2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400
Db       2341 TCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAACTGCTGCAG 2400

Qy       2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460
Db       2401 GTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGGAGGAAGCC 2460

Qy       2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
Db       2461 AGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520

Qy       2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580
Db       2521 GCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAGCATTAGTT 2580

Qy       2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640
Db       2581 GAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGATCGGACAG 2640

Qy       2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700
Db       2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAGCGCACCCG 2700

Qy       2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760
Db       2701 CTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACGCGGTCGAA 2760

Qy       2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
Db       2761 CCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAGAATTCCTA 2820

Qy       2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880
Db       2821 GCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACCGCAAACTA 2880

Qy       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940
Db       2881 TACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACAAGGTTACA 2940

Qy       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000
Db       2941 AAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTTGCGTTAAG 3000

Qy       3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060
Db       3001 AAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCTATCATGAG 3060

Qy       3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120
Db       3061 CTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAACAATAGGA 3120

Qy       3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180
Db       3121 GTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCACGGCACGA 3180

Qy       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Db       3181 GATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240

Qy       3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300
Db       3241 CTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACGGATGCCAC 3300

Qy       3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360
Db       3301 AAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAGCACTACTT 3360

Qy       3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Db       3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACCCCATGCAA 3420

Qy       3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480
Db       3421 TGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAAAAGACATA 3480

Qy       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Db       3481 TGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540

Qy       3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600
Db       3541 GTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGAAGAACATT 3600

Qy       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660
Db       3601 GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGACATGTTTC 3660

Qy       3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720
Db       3661 CGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGACAGCCGCG 3720

Qy       3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
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Db      3721 GCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCAATGAAAAC 3780
Qy      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Db      3781 CCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTGAGGACAGG 3840
Qy      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Db      3841 CTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACATACCTAAA 3900
Qy      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Db      3901 GGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAATTGCTGCA 3960
Qy      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Db      3961 ATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTTGCTGGGCG 4020
Qy      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Db      4021 AAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCCAGTGGAGC 4080
Qy      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
Db      4081 GAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCTTAGACGTA 4140
Qy      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
Db      4141 ATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAACAGAGCATC 4200
Qy      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
Db      4201 CCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACAACAGCCCA 4260
Qy      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
Db      4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTAGATTTCCG 4320
Qy      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
Db      4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAACCAGAGTT 4380
Qy      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
Db      4381 ATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCTTAGTCCCC 4440
Qy      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
Db      4441 GAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCAAACACCAC 4500
Qy      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
Db      4501 TCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCGAATGGATC 4560
Qy      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
Db      4561 GCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG 4620
Qy      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
Db      4621 CAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACCACCACTTT 4680
Qy      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
Db      4681 CAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCCTGAATTGT 4740
Qy      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
Db      4741 TTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCAACAGTGAG 4800
Qy      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
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Db      4801 GACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAGATTGT 4860
Qy      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
Db      4861 GTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCCGTACACGG 4920
Qy      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
Db      4921 CAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTACAAGAGAT 4980
Qy      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
Db      4981 GGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACTGTCAAGAG 5040
Qy      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
Db      5041 GAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCTGCCGTGCC 5100
Qy      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
Db      5101 ATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCACCGCAAGA 5160
Qy      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
Db      5161 ATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCCGGAAGCAC 5220
Qy      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
Db      5221 CCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAGACTTAGTA 5280
Qy      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
Db      5281 AATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTTACGCAGCC 5340
Qy      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
Db      5341 GGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACAGAACTGAC 5400
Qy      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
Db      5401 GCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACGCGGCACTC 5460
Qy      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
Db      5461 CAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACGATGAGTTA 5520
Qy      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
Db      5521 GTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTACAAAAGGA 5580
Qy      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
Db      5581 AAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACATGGCGGAG 5640
Qy      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
Db      5641 ATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCTACATATTG 5700
Qy      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
Db      5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGTCGTCTAGC 5760
Qy      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
Db      5761 CCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA 5820
Qy      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
Db      5821 CTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTCCTAAGCAC 5880
Qy      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
Db      5881 AAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATCCGCACACT 5940
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Qy       5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000
Db       5941 CCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCGCTCCTCCT 6000

Qy       6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060
Db       6001 GCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC 6060

Qy       6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120
Db       6061 ACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGGCTCACTT 6120

Qy       6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180
Db       6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGTCGTCAGGA 6180

Qy       6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240
Db       6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTCATGCCGTC 6240

Qy       6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300
Db       6241 CAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGGCAGCGGCA 6300

Qy       6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360
Db       6301 AGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTCTTTTGGT 6360

Qy       6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420
Db       6361 GGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGGCAGCGGTA 6420

Qy       6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480
Db       6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTTCCGACGGA 6480

Qy       6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
Db       6481 GAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTGGATCATTT 6540

Qy       6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600
Db       6541 GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC 6600

Qy       6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660
Db       6601 AAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGGTAGGTGGG 6660

Qy       6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720
Db       6661 TACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTCTGCAGAAC 6720

Qy       6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780
Db       6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCCCGGTGCTC 6780

Qy       6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840
Db       6781 GACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCGAAGCCAAC 6840

Qy       6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
Db       6841 AAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTGAGCGACTA 6900

Qy       6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960
Db       6901 CTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATAAGATCACC 6960

Qy       6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
Db       6961 TATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCACAGTTCGCT 7020
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Qy       7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Db       7021 GTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080

Qy       7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140
Db       7081 ACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCCTGGATACT 7140

Qy       7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200
Db       7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATAGAGCCCCG 7200

Qy       7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260
Db       7201 AATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGCTCATTGCC 7260

Qy       7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320
Db       7261 GCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGGACTCAGCG 7320

Qy       7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380
Db       7321 ACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGGAGGAGTTC 7380

Qy       7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440
Db       7381 GCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTAGACTGAAA 7440

Qy       7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500
Db       7441 GGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGCAAGAAGTG 7500

Qy       7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560
Db       7501 CCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAGGCACGAAA 7560

Qy       7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620
Db       7561 CACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGGCGACTGCT 7620

Qy       7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680
Db       7621 TACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGCTTCCAAAC 7680

Qy       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740
Db       7681 ATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAGAACACTTC 7740

Qy       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800
Db       7741 AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCCAAGACGAC 7800

Qy       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860
Db       7801 GCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAACCACTACTC 7860

Qy       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920
Db       7861 GACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGGGTACTCGT 7920

Qy       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980
Db       7921 TTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCAACACAGTT 7980

Qy       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040
Db       7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCAGATGTGCA 8040

Qy       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Db       8041 GCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAATGGCTGAG 8100

Qy       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160
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Db       8101 AGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCGGTGAGAGA 8160

Qy       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8161 CCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAGCGTGCCGC 8220

Qy       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8221 GTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCGACGACGAG 8280

Qy       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8281 CAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTAGAGTAGGT 8340

Qy       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8341 ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATATTACACCT 8400

Qy       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8401 GTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG 8460

Qy       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8461 GAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCATCTGACTAA 8520

Qy       8521 TACTACAACACCACCACCT 8539
             ||||||||||||||||||||
Db       8521 TACTACAACACCACCACCT 8539
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RESULT 5
ADL71890
ID ADL71890 standard; cDNA; 13068 BP.
XX
AC ADL71890;
XX
DT 20-MAY-2004 (first entry)
XX
DE Temperature inducible alphavirus vector pCytTs2.1.
XX
KW Gene expression; vector; pCytTS2.1; ss.
XX
OS Cytomegalovirus.
OS Alphavirus.
OS Chimeric.
XX
PN WO2004018506-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-EP009291.
XX
PR 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Ivanova L, Renner WA, Saudan P;
XX
DR WPI; 2004-226795/21.
XX
PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX
PS Example 1; SEQ ID NO 2; 112pp; English.
XX
CC The present sequence is that of the tightly regulated temperature
CC inducible alphavirus expression system pCytTS2.1 containing a
CC cytomegalovirus (CMV). The vector can be used to drive transcription of
CC mRNA from a nucleic acid molecule of the invention. A claimed nucleic
CC acid molecule comprises: (A) a first polynucleotide element which encodes
CC an RNA molecule comprising (a) at least one cis-acting sequence element,
CC (b) a first nucleotide sequence comprising a first open reading frame,
CC the first open reading frame having a nucleotide sequence encoding an RNA
CC -dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, i.e. the cis-acting replication origin oriP and the cis- or trans-
CC acting gene product EBNA-1 with pCysTS. Due to the presence of OriP and
CC EBNA-1, the novel vector is maintained episomally in the form of several
CC DNA copies in cell nuclei. These multiple DNA copies may be transcribed
CC from the CMV promoter into CysTS2.1 RNA replicons, but remain inactive
CC unless cells are shifted to a certain temperature. Only after temperature
CC induction does replicon replication occur, followed by RNA accumulation
CC and translation in the cell cytoplasm, and production of the polypeptide
CC of interest.
XX
SQ Sequence 13068 BP; 3555 A; 3379 C; 3204 G; 2930 T; 0 U; 0 Other;

Query Match 89.7%; Score 7657.2; DB 12; Length 13068;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7642; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        929 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 988

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        989 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1048

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1108

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1168

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1169 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATATGCCAGTA 1228

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1229 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1288

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1348

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1408

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1468
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Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1469 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1528

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1529 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1588

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1589 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1648

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1649 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1708

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1709 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1768

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1769 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1828

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1829 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1888

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1889 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1948

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1949 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2008

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2009 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2068

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2069 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2128

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2129 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2188

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2189 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2248

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2249 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2308

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2309 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2368

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2369 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2428

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2429 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2488

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2489 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2548

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2549 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2608

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2609 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2668

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2669 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2728

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2729 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2788

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2789 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2848

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2849 GCAAACTATACCACATTGCCATGCATGGCCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2908

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2909 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2968

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2969 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3028

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3029 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3088

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3089 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3148

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3149 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3208

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3209 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3268

Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3269 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3328

Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3329 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3388

Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3389 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3448

Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3449 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3508

Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3509 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3568

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3569 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3628

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      3629 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3688
Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db      3689 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3748
Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
Db      3749 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3808
Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
Db      3809 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCTCACTAACA 3868
Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
Db      3869 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3928
Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
Db      3929 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3988
Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
Db      3989 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4048
Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
Db      4049 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4108
Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
Db      4109 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4168
Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
Db      4169 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4228
Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
Db      4229 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4288
Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
Db      4289 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4348
Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
Db      4349 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4408
Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
Db      4409 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCGAAAAATTCTTGAACCAGTTCA 4468
Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
Db      4469 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4528
Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
Db      4529 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4588
Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
Db      4589 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4648
Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db      4649 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4708
Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
Db      4709 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4768
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Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
Db      4769 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4828
Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
Db      4829 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4888
Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
Db      4889 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4948
Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
Db      4949 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5008
Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
Db      5009 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5068
Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
Db      5069 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5128
Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
Db      5129 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5188
Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
Db      5189 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5248
Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db      5249 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5308
Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
Db      5309 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5368
Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
Db      5369 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5428
Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
Db      5429 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5488
Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
Db      5489 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5548
Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
Db      5549 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5608
Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
Db      5609 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5668
Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
Db      5669 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5728
Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db      5729 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5788
Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
Db      5789 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5848
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Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5849 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5908

Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5909 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5968

Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5969 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6028

Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6029 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6088

Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6089 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6148

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6149 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6208

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6209 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6268

Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6269 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6328

Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6329 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6388

Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6389 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6448

Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6449 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6508

Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6509 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6568

Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6569 CTCTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6628

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6629 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6688

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6689 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6748

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6749 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6808

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6809 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6868

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6869 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6928

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6929 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6988

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6989 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7048

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7049 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7108

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7109 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7168

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
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Db       7169 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7228

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
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Db       7229 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7288

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7289 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7348

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7349 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7408

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7409 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7468

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
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Db       7469 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7528

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7529 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7588

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7589 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7648

Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7649 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7708

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7709 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7768

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7769 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7828

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7829 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7888

Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
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Db       7889 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7948

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7949 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8008

Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       8009 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8068

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8069 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8128

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8129 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8188

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8189 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8248

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8249 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8308

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8309 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8368

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8369 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8428

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8429 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8488

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             |||||||||||| ||||||||||||||
Db       8489 CTGACTAATACCACAACACCACCACCT 8515
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RESULT 6
ADL71909
ID ADL71909 standard; cDNA; 15081 BP.
XX
AC ADL71909;
XX
DT 20-MAY-2004 (first entry)
XX
DE Expression vector pCytTs-OriP.
XX
KW Gene expression; vector; pCytTS; ss.
XX
OS Alphavirus.
OS Human herpesvirus 4.
OS Chimeric.
XX
PN WO2004018506-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-EP009291.
XX
PR 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Ivanova L, Renner WA, Saudan P;
XX
DR WPI; 2004-226795/21.
XX
PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX
PS Example 2; SEQ ID NO 21; 112pp; English.
XX
CC The present sequence is that of expression vector pCytTs-OriP. A claimed
CC nucleic acid molecule comprises: (A) a first polynucleotide element which
CC encodes an RNA molecule comprising (a) at least one cis-acting sequence
CC element, (b) a first nucleotide sequence comprising a first open reading
CC frame, the first open reading frame having a nucleotide sequence encoding
CC an RNA-dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, e.g. the cis-acting replication origin oriP from Epstein Barr
CC virus, with pCysTS ADL71889, creating pCytTs-OriP. Due to the presence of
CC OriP, the novel vector is maintained episomally in the form of several
CC DNA copies in cell nuclei. These multiple DNA copies may be transcribed
CC from a Rous sarcoma virus or cytomegalovirus promoter into pCysTS RNA
CC replicons, but remain inactive unless cells are shifted to a certain
CC temperature. Only after temperature induction does replicon replication
CC occur, followed by RNA accumulation and translation in the cell
CC cytoplasm, and production of the polypeptide of interest.
XX
SQ Sequence 15081 BP; 4101 A; 3826 C; 3676 G; 3478 T; 0 U; 0 Other;

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  Query Match             89.7%;  Score 7657.2;  DB 12;  Length 15081;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7642;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        929 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 988

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        989 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1048

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1108

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1168

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1169 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATATGCCAGTA 1228

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1229 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1288

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1348

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1408

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1468
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Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1469 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1528

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1529 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1588

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1589 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1648

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1649 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1708

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1709 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1768

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1769 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1828

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1829 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1888

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1889 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1948

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1949 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2008

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2009 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2068

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2069 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2128

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2129 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2188

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2189 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2248

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2249 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2308

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2309 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2368

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2369 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2428

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2429 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2488

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2489 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2548

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2549 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2608

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2609 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2668

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2669 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2728

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2729 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2788

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2789 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2848

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2849 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2908

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2909 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2968

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2969 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3028

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3029 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3088

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3089 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3148

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3149 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3208

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3209 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3268

Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3269 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3328

Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3329 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3388

Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3389 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3448

Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3449 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3508

Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3509 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3568

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3569 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3628

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      3629 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3688

Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3689 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3748

Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3749 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3808

Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db      3809 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCTCACTAACA 3868

Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3869 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3928

Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3929 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3988

Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3989 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4048

Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4049 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4108

Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4109 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4168

Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4169 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4228

Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4229 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4288

Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4289 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4348

Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4349 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4408

Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db      4409 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCGAAAAATTCTTGAACCAGTTCA 4468

Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4469 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4528

Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4529 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4588

Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4589 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4648

Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4649 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4708

Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4709 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4768
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Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4769 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4828

Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4829 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4888

Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4889 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4948

Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4949 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5008

Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5009 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5068

Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5069 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5128

Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5129 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5188

Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5189 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5248

Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5249 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5308

Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5309 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5368

Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5369 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5428

Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5429 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5488

Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5489 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5548

Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5549 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5608

Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5609 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5668

Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5669 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5728

Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5729 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5788

Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5789 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5848
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Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
Db       5849 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5908

Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
Db       5909 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5968

Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
Db       5969 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6028

Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
Db       6029 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6088

Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
Db       6089 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6148

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
Db       6149 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6208

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
Db       6209 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6268

Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
Db       6269 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6328

Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
Db       6329 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6388

Qy       6413 CAGCGGTACAACCCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
Db       6389 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6448

Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
Db       6449 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6508

Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
Db       6509 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6568

Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
Db       6569 CTCTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6628

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
Db       6629 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6688

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
Db       6689 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6748

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
Db       6749 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6808

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
Db       6809 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6868

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
Db       6869 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6928

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012

Db       6929 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6988

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
Db       6989 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7048

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
Db       7049 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7108

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
Db       7109 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7168

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
Db       7169 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7228

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
Db       7229 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7288

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
Db       7289 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7348

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
Db       7349 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7408

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
Db       7409 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7468

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
Db       7469 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7528

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
Db       7529 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7588

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
Db       7589 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7648

Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
Db       7649 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7708

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
Db       7709 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7768

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
Db       7769 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7828

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
Db       7829 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7888

Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
Db       7889 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7948

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
Db       7949 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8008

Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Db       8009 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8068

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8069 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8128

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8129 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8188

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8189 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8248

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8249 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8308

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8309 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8368

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8369 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8428

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8429 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8488

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             |||||||||||  ||||||||||||||
Db       8489 CTGACTAATACCACAACACCACCACCT 8515
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RESULT 7
ADL71910
ID ADL71910 standard; cDNA; 17753 BP.
XX
AC ADL71910;
XX
DT 20-MAY-2004 (first entry)
XX
DE Expression vector pCytTs-OPE.
XX
KW Gene expression; vector; pCytTS; ss.
XX
OS Alphavirus.
OS Human herpesvirus 4.
OS Chimeric.
XX
PN WO2004018506-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-EP009291.
XX
PR 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Ivanova L, Renner WA, Saudan P;
XX
DR WPI; 2004-226795/21.
XX
PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX
PS Example 2; SEQ ID NO 22; 112pp; English.
XX
CC The present sequence is that of expression vector pCytTs-OPE. A claimed
CC nucleic acid molecule comprises: (A) a first polynucleotide element which
CC encodes an RNA molecule comprising (a) at least one cis-acting sequence
CC element, (b) a first nucleotide sequence comprising a first open reading
CC frame, the first open reading frame having a nucleotide sequence encoding
CC an RNA-dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, e.g. the cis-acting replication origin oriP and replication
CC initiation factor EBNA1 from Epstein Barr virus, with pCysTS ADL71889,
CC creating pCytTs-ORE. Due to the presence of OriP and EBNA1, the novel
CC vector is maintained episomally in the form of several DNA copies in cell
CC nuclei. These multiple DNA copies may be transcribed from a Rous sarcoma
CC virus or cytomegalovirus promoter into pCysTS RNA replicons, but remain
CC inactive unless cells are shifted to a certain temperature. Only after
CC temperature induction does replicon replication occur, followed by RNA
CC accumulation and translation in the cell cytoplasm, and production of the
CC polypeptide of interest.
XX
SQ Sequence 17753 BP; 4502 A; 4902 C; 4209 G; 4140 T; 0 U; 0 Other;

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  Query Match           89.7%;  Score 7657.2;  DB 12;  Length 17753;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 7642;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 928

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        929 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 988

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        989 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1048

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1108

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1168

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1169 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATATGCCAGTA 1228

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1229 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1288

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1348

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1408

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1468
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Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1469 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1528

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1529 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1588

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1589 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1648

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1649 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1708

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1709 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1768

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1769 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1828

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1829 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1888

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1889 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1948

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1949 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2008

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2009 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2068

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2069 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2128

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2129 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2188

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2189 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2248

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2249 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2308

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2309 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2368

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2369 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2428

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2429 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2488

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2489 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2548
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Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2549 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2608

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2609 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2668

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2669 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2728

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2729 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2788

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2789 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2848

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2849 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2908

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2909 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2968

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2969 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3028

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3029 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3088

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3089 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3148

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3149 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3208

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3209 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3268

Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3269 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3328

Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3329 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3388

Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3389 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3448

Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3449 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3508

Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3509 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3568

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3569 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3628

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
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Db      3629 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3688
Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db      3689 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3748
Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
Db      3749 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3808
Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
Db      3809 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCTCACTAACA 3868
Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
Db      3869 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3928
Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
Db      3929 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3988
Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
Db      3989 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4048
Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
Db      4049 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4108
Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
Db      4109 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4168
Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
Db      4169 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4228
Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
Db      4229 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4288
Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
Db      4289 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4348
Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
Db      4349 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4408
Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
Db      4409 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCGAAAAATTCTTGAACCAGTTCA 4468
Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
Db      4469 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4528
Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
Db      4529 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4588
Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
Db      4589 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4648
Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db      4649 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4708
Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
Db      4709 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4768
Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
Db      4769 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4828
Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
Db      4829 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4888
Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
Db      4889 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4948
Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
Db      4949 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5008
Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
Db      5009 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5068
Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
Db      5069 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5128
Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
Db      5129 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5188
Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
Db      5189 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5248
Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db      5249 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5308
Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
Db      5309 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5368
Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
Db      5369 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5428
Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
Db      5429 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5488
Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
Db      5489 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5548
Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
Db      5549 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5608
Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
Db      5609 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5668
Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
Db      5669 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5728
Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db      5729 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5788
Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
Db      5789 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5848
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Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5849 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5908

Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5909 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5968

Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5969 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6028

Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6029 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6088

Qy       6113 GCTCACTTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6089 GCTCACTTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6148

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6149 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6208

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6209 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6268

Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6269 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6328

Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6329 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6388

Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6389 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6448

Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6449 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6508

Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6509 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6568

Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6569 CTCTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6628

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6629 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6688

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6689 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6748

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6749 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6808

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6809 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6868

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6869 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6928
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Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6929 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6988

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6989 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7048

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7049 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7108

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7109 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7168

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7169 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7228

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7229 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7288

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7289 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAAATATGCATGTAATGACGAGTATTGGG 7348

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7349 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7408

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7409 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7468

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7469 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7528

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7529 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7588

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7589 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7648

Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7649 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7708

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7709 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7768

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7769 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7828

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7829 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7888

Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7889 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7948

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7949 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8008

Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Db       8009 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8068

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8069 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8128

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8129 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8188

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8189 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8248

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8249 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8308

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8309 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8368

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8369 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8428

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8429 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8488

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             |||||||||| ||||||||||||||||
Db       8489 CTGACTAATACCACAACACCACCACCT 8515
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RESULT 8
AAX77354
ID AAX77354 standard; DNA; 9951 BP.
XX
AC AAX77354;
XX
DT 09-AUG-1999 (first entry)
XX
DE Polynucleotide sequence of pSinRep 5.
XX
KW Nucleic acid identification; exogenous protein; gene sorting;
KW growth factor; membrane receptor; sindbis virus; ss.
XX
OS Synthetic.
XX
PN WO9925876-A1.
XX
PD 27-MAY-1999.
XX
PF 17-NOV-1998; 98WO-US024520.
XX
PR 17-NOV-1997; 97US-00972218.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
PI Bailey JE, Renner WA, Orberger GH, Koller D;
XX
DR WPI; 1999-357620/30.
XX
PT Isolating genes encoding proteins with selected properties, useful for
PT identifying therapeutic agents or targets.
XX
PS Disclosure; Fig 11A-C; 136pp; English.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing a population of eukaryotic host cells, culturing the
CC cells under suitable conditions and identifying cells that contain the
CC recombinant nucleic acid. The method is used to sort genes according to
CC the type of proteins they express, and also to identify new ligand/
CC receptor interactions. Typical applications of the nucleic acid and the
CC exogenous protein are in isolation of new growth factors, cytokines,
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
CC which may be useful as therapeutic agents or therapeutic targets, e.g.
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
CC proliferation or metabolic processes etc. The protein can also be used to
CC screen for specific modulators. The nucleic acid can also be used as
CC sources of therapeutic antisense or ribozyme sequences. The method allows
CC the protein (rather than a partial DNA sequence) to be isolated and,
CC since a wide range of cells can be used, they can be expressed with the
CC correct glycosylation pattern
XX
SQ Sequence 9951 BP; 2852 A; 2461 C; 2464 G; 2174 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 2; Length 9951;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780
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Qy      1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy      1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy      1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy      1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy      1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy      1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy      2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

Qy      2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy      2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy      2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy      2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy      2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500

Qy      2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy      2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy      2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy      2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy      2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800

Qy      2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860

Qy      2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920

Qy      2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980

Qy      2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy      2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy      2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160

Qy      3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220

Qy      3113 CAATAGGAGTGATAGGCACACCGGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 CAATAGGAGTGATAGGCACACCGGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy      3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy      3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

Qy      3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy      3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy      3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy      3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy      3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy      3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy      3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000
Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060
Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120
Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180
Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240
Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300
Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360
Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420
Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480
Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540
Qy       4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600
Qy       4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660
Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720
Qy       4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
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Db       3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780
Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840
Qy       4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             |||||||  | |||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900
Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960
Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020
Qy       4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140
Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200
Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260
Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320
Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380
Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440
Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500
Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560
Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620
Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680
Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740
Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800
Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
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Db       4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860
Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920
Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980
Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040
Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100
Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160
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Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220

Qy       6113 GCTCACTTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCACTTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400

Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460

Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520

Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580

Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640

Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700

Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780

Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020

Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140

Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             ||||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
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RESULT 9
AAA90386
ID AAA90386 standard; DNA; 9951 BP.
XX
AC AAA90386;
XX
DT 10-JAN-2001 (first entry)
XX
DE Sindbis expression vector pSinRep5 DNA sequence.
XX
KW Nucleic acid identification; exogenous protein; drug screening;
KW recombinant expression; pSinRep5; mammalian expression system; cyclic;
KW circular; ds.
XX
OS Synthetic.
OS Sindbis virus.
XX
PN JP2000189173-A.
XX
PD 11-JUL-2000.
XX
PF 23-AUG-1999; 99JP-00236220.
XX
PR 17-NOV-1998; 98US-00193707.
PR 17-NOV-1998; 98WO-US024520.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
DR WPI; 2000-551637/51.
XX
PT Identifying a recombinant nucleic acid to identify and isolate various
PT cellular proteins, comprises culturing a composition comprising
PT eukaryotic host cells and identifying a cell comprising recombinant
PT nucleic acid.
XX
PS Example 7; Fig 11A-C; 56pp; Japanese.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property.The method
CC comprises preparing populations of eukaryotic host cells, where each cell
CC comprises an expression vector encoding a different exogenous protein.
CC The host cells are cultured under suitable conditions and the nucleic
CC acid which encodes the exogenous protein is identified. The method is
CC useful for the identification and isolation of proteins with a selected
CC property. Typical applications of the nucleic acid and the exogenous
CC protein are in isolation of new growth factors, cytokines, membrane
CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may
CC be useful as therapeutic agents or therapeutic targets, e.g., pro-
CC apoptotic or tumour suppressing proteins, regulators of cell
CC proliferation or of metabolic processes. The protein can also be used to
CC screen for ligands and specific modulators of activity. The method of the
CC invention allows the direct cloning of full length cDNAs in one step. It
CC facilitates direct expression of the protein without the need to perform
CC further procedures such as subcloning and establishment of a cell line
CC for protein production. The method allows a protein of interest (rather
CC than a partial DNA sequence) to be isolated and, since a wide range of
CC cell types can be used, they can be expressed in a correctly folded and
CC glycosylated form. The present sequence represents the Sindbis expression
CC vector pSinRep5 which was used in the exemplifications of the invention.
CC This patent is related to WO9925876
XX
SQ Sequence 9951 BP; 2852 A; 2461 C; 2464 G; 2174 T; 0 U; 0 Other;

  Query Match   89.4%; Score 7637.4; DB 3; Length 9951;
  Best Local Similarity   99.9%; Pred. No. 0;
  Matches 7641; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840
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Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060
Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120
Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
Db       3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180
Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
Db       3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240
Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
Db       3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300
Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
Db       3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360
Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
Db       3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420
Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
Db       3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480
Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
Db       3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540
Qy       4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
Db       3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600
Qy       4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
Db       3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660
Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
Db       3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720
Qy       4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
Db       3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780
Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db       3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840
Qy       4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
Db       3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900
Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
Db       3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960
Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
Db       3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020
Qy       4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
Db       4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080
Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
Db       4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140
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Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
Db       4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200
Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
Db       4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260
Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
Db       4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320
Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
Db       4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380
Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db       4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440
Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
Db       4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500
Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
Db       4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560
Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
Db       4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620
Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
Db       4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680
Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
Db       4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740
Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
Db       4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800
Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
Db       4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860
Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db       4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920
Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
Db       4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980
Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
Db       4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040
Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
Db       5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100
Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
Db       5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160
Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
Db       5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220
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Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy      6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340

Qy      6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400

Qy      6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460

Qy      6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520

Qy      6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580

Qy      6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640

Qy      6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700

Qy      6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760

Qy      6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820

Qy      6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880

Qy      6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940

Qy      6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

Qy      6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060

Qy      6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120

Qy      7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180

Qy      7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             |||||||||||||||||||||||||||||||||||||||||| ||||||||| ||||||
Db      6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240

Qy      7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300

Qy      7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360

Qy      7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420

Qy      7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480

Qy      7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540

Qy      7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600

Qy      7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660

Qy      7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720

Qy      7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780

Qy      7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840

Qy      7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900

Qy      7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960

Qy      7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020

Qy      7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080

Qy      7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140

Qy      8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200

Qy      8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260

Qy      8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320

Qy      8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

Qy      8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             ||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
```

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RESULT 10
AAD04742
ID   AAD04742 standard; DNA; 9951 BP.
XX
AC   AAD04742;
XX
DT   17-JUL-2001  (first entry)
XX
DE   Alphaviral vector pSinRep5 DNA.
XX
KW   pSinRep5; alphaviral vector; vaccine; therapy; cancer; antiparasitic;
KW   antimalarial; anticancer; anti-HIV; antiviral; infectious disease;
KW   Human immunodeficiency virus; HIV; influenza; passive immunisation;
KW   carcinoma; liver; skin; stomach; ovarian tumour; ds.
XX
OS   Synthetic.
XX
PN   WO200130989-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-IB001557.
XX
PR   27-OCT-1999;  99US-0161796P.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA   (RENN/) RENNER W A.
PA   (NIEB/) NIEBA L.
XX
PI   Renner WA, Nieba L;
XX
DR   WPI; 2001-308631/32.
XX
PT   Preparing alphaviral vectors with mutations in a selected gene, for use
PT   as vaccines, particularly against pathogens that mutate rapidly,
PT   comprises replicating in the presence of a nucleoside analog.
XX
PS   Claim 4; Fig 4; 103pp; English.
XX
CC   The present invention relates to a method for preparing viral vectors
CC   which comprises inserting a gene of interest into an alphaviral vector
CC   such as pCYTts, pSinRep5 and replicating the vector in the presence of
CC   alphaviral replicase and nucleoside analogues (5'azacytidine (AZT), FU-
CC   5' fluorouridine) to produce a modified gene of interest. The replication
CC   is repeated until the modified gene in 90 % of the vector population
CC   contain a mutation in the modified gene which is 90-99 % identical with
CC   the gene of interest. The vector populations are used in vaccines for
CC   treatment or prevention of a wide variety of infectious diseases (viral
CC   or parasitic, e.g. human immuno deficiency virus (HIV), influenza,
CC   Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach
CC   carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the
CC   mutant populations will therefore be effective against viral escape
CC   mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins
CC   are correctly glycosylated. Antisera raised against the vaccines can be
CC   used for passive immunisation. The present DNA sequence is an alphaviral
CC   vector pSinRep5. pSinRep5 contains nucleic acid which encodes a wild-type
CC   alphaviral replicase. Thus, this replicase in cytopathic and eukaryotic
CC   cells which express it will generally become non-viable within 24 hours
CC   after initiation of expression
XX
SQ   Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;
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  Query Match             89.4%;  Score 7637.4;  DB 4;  Length 9951;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 7641;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
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Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960
Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020
Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080
Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140
Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
Db       1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200
Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
Db       1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260
Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320
Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380
Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440
Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
Db       1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500
Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560
Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620
Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
Db       1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680
Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
Db       1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740
Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
Db       1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800
Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
Db       1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860
Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
Db       1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920
Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
Db       1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980
Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
Db       1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040
Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
Db       2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100
Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
Db       2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160
Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
Db       2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220
Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
Db       2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280
Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
Db       2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340
Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
Db       2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400
Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
Db       2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460
Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
Db       2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520
Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
Db       2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580
Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
Db       2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640
Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
Db       2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700
Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
Db       2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760
Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
Db       2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820
Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db       2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880
Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
Db       2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940
Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
Db       2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000
Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060
Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120
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Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780

Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             |||||||  | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260

Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380

Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500

Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800

Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860

Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920

Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980

Qy      5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040

Qy      5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100

Qy      5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160

Qy      6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220

Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy      6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
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Db      5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340
Qy      6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
Db      5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400
Qy      6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
Db      5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460
Qy      6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
Db      5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520
Qy      6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
Db      5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580
Qy      6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
Db      5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640
Qy      6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
Db      5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
Qy      6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
Db      5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760
Qy      6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
Db      5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820
Qy      6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
Db      5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880
Qy      6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
Db      5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940
Qy      6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
Db      5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000
Qy      6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
Db      6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060
Qy      6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
Db      6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120
Qy      7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
Db      6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180
Qy      7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
Db      6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240
Qy      7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
Db      6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300
Qy      7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
Db      6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360
Qy      7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
Db      6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420
Qy      7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
Db      6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480
Qy      7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
Db      6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540
Qy      7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
Db      6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600
Qy      7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
Db      6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660
Qy      7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
Db      6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720
Qy      7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
Db      6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
Qy      7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
Db      6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840
Qy      7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
Db      6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900
Qy      7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
Db      6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960
Qy      7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
Db      6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020
Qy      7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
Db      7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080
Qy      7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
Db      7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140
Qy      8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
Db      7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200
Qy      8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
Db      7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260
Qy      8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
Db      7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320
Qy      8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
Db      7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380
Qy      8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
Db      7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440
Qy      8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
Db      7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500
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Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             |||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
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RESULT 11
ABN86686
ID ABN86686 standard; DNA; 9951 BP.
XX
AC ABN86686;
XX
DT 05-NOV-2002 (first entry)
XX
DE Nucleotide sequence of a SINrep5 self replicating replicon.
XX
KW Major histocompatibility complex; MHC; antigen presenting cell; APC;
KW antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic;
KW cancer; viral infection; ds.
XX
OS Synthetic.
XX
PN WO200261113-A2.
XX
PD 08-AUG-2002.
XX
PF 01-FEB-2002; 2002WO-US002598.
XX
PR 01-FEB-2001; 2001US-0265334P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-619261/66.
XX
PT Nucleic acid molecule encoding a fusion polypeptide that promotes
PT processing via the Major Histocompatibility Complex class I pathway
PT and/or promotes activity of an antigen presenting cell, useful as vaccine
PT for cancer and viral infections.
XX
PS Claim 27; Page 23-25; 127pp; English.
XX
CC The invention relates to a new nucleic acid molecule (I) encoding a
CC fusion polypeptide useful as a vaccine composition. (I) comprises a first
CC nucleic acid sequence encoding a first polypeptide or peptide that
CC promotes processing via the Major Histocompatibility Complex (MHC) class
CC I pathway (MHC-I-PP) and/or promotes development or activity of an
CC antigen presenting cell (APC). The second nucleic acid sequence is linked
CC in frame to the first nucleic acid sequence or to a linker nucleic acid
CC sequence and encodes an antigenic polypeptide or peptide. The methods and
CC compositions of the present invention are useful as therapeutic vaccine
CC for cancer and for major viral infections, such as hepatoma and cervical
CC cancer, that cause morbidity and mortality. They can also be used in
CC treating animal diseases, such as equine herpesvirus, bovine viruses,
CC Marek's disease, retroviral and lentiviral diseases and rabies, in the
CC veterinary medicine context. The present sequence represents the
CC nucleotide sequence of a SINrep5 self replicating replicon
XX
SQ Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 6; Length 9951;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
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Db      1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140
Qy      2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
Db      1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200
Qy      2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
Db      1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260
Qy      2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
Db      1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320
Qy      2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
Db      1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380
Qy      2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
Db      1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440
Qy      2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
Db      1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500
Qy      2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
Db      1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560
Qy      2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
Db      1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620
Qy      2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
Db      1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680
Qy      2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
Db      1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740
Qy      2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
Db      1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800
Qy      2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
Db      1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860
Qy      2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
Db      1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920
Qy      2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
Db      1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980
Qy      2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
Db      1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040
Qy      2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
Db      2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100
Qy      2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
Db      2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160
Qy      3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
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Db      2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220
Qy      3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
Db      2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280
Qy      3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
Db      2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340
Qy      3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
Db      2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400
Qy      3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
Db      2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460
Qy      3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
Db      2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520
Qy      3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
Db      2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580
Qy      3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
Db      2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640
Qy      3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
Db      2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700
Qy      3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
Db      2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760
Qy      3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
Db      2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820
Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db      2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880
Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
Db      2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940
Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
Db      2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000
Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
Db      3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060
Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
Db      3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120
Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
Db      3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180
Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
Db      3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240
Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
Db      3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300
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Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780

Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             |||||||  | ||| ||||||||||||||||||||||||||||||||||||||||||||
Db      3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260

Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380
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Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500

Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800

Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860

Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920

Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980

Qy      5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040

Qy      5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100

Qy      5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160

Qy      6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220

Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy      6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340

Qy      6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400

Qy      6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460

Qy      6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
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Db      5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520
Qy      6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
Db      5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580
Qy      6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
Db      5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640
Qy      6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
Db      5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
Qy      6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
Db      5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760
Qy      6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
Db      5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820
Qy      6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
Db      5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880
Qy      6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
Db      5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940
Qy      6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
Db      5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000
Qy      6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
Db      6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060
Qy      6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
Db      6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120
Qy      7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
Db      6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180
Qy      7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
Db      6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240
Qy      7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
Db      6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300
Qy      7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
Db      6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360
Qy      7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
Db      6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420
Qy      7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
Db      6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480
Qy      7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
Db      6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540
Qy      7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
Db      6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600
Qy      7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
Db      6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660
Qy      7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
Db      6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720
Qy      7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
Db      6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
Qy      7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
Db      6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840
Qy      7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
Db      6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900
Qy      7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
Db      6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960
Qy      7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
Db      6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020
Qy      7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
Db      7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080
Qy      7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
Db      7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140
Qy      8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
Db      7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200
Qy      8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
Db      7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260
Qy      8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
Db      7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320
Qy      8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
Db      7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380
Qy      8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
Db      7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440
Qy      8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
Db      7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500
Qy      8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
Db      7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560
Qy      8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
Db      7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620
Qy      8513 CTGACTAATACTACAACACCACCACCT 8539
Db      7621 CTGACTAATACTACAACACCACCACCT 7647
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RESULT 12
ABV73174
ID ABV73174 standard; DNA; 9951 BP.
XX
AC ABV73174;
XX
DT 08-JAN-2003 (first entry)
XX
DE Nucleotide sequence of Sinrep5 self replicating replicon.
XX
KW Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
KW hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; ds.
XX
OS Sindbis virus.
XX
PN WO200274920-A2.
XX
PD 26-SEP-2002.
XX
PF 18-MAR-2002; 2002WO-US008033.
XX
PR 16-MAR-2001; 2001US-0276854P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-740856/80.
XX
PT New nucleic acid molecule encoding an antigenic fusion polypeptide useful
PT as vaccines for enhancing or inducing immune responses, primarily
PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as
PT tumor or viral antigens.
XX
PS Disclosure; Page 56-58; 93pp; English.
XX
CC The invention relates to a nucleic acid molecule that encodes a fusion
CC polypeptide, comprising a first nucleic acid sequence encoding a
CC polypeptide that comprises at least one immunogenicity-potentiating
CC polypeptide, optionally, fused in frame with the nucleic acid, a linker
CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked
CC in frame to them, and that encodes an antigenic peptide or polypeptide.
CC The nucleic acid molecule, polypeptides and vectors are useful as
CC vaccines for enhancing immune responses, primarily cytotoxic T
CC lymphocytes (CTL) responses to specific antigens such as tumour or viral
CC antigens, and for inhibiting growth or preventing re-growth of a tumour.
CC The packaging cell line is useful for generating alphavirus replicon
CC particles without contamination from replicon-competent virus. The
CC pathogenic organisms include viruses such as human papilloma virus (HPV),
CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
CC Epstein Barr virus and herpes simplex virus, intracellular parasites such
CC as malaria, and bacteria that grow intracellularly such as mycobacteria
CC and listeria. The present sequence represents the nucleotide sequence of
CC the sindbis virus RNA replicon vector Sinrep5, a self replicating
CC replicon
XX
SQ Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 6; Length 9951;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy      2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy      2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy      2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy      2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500

Qy      2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy      2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy      2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy      2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy      2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800

Qy      2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860

Qy      2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920

Qy      2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980

Qy      2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy      2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy      2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160

Qy      3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220

Qy      3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy      3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340
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Qy      3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

Qy      3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy      3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy      3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy      3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy      3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy      3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy      3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420
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Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780

Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             |||||||  | ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260

Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380

Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500

Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800

Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860

Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920

Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980

Qy      5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040

Qy      5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100

Qy      5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160

Qy      6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220

Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy      6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340

Qy      6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400

Qy      6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460

Qy      6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520

Qy      6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580

Qy      6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640
Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760
Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820
Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880
Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940
Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000
Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060
Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120
Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180
Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             |||||||||||||||||||||||||||||||||||||||||| ||||||||| ||||
Db       6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240
Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300
Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360
Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420
Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480
Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540
Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600
Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660
Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720
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Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840
Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900
Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960
Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020
Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080
Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140
Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200
Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260
Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320
Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380
Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440
Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500
Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560
Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620
Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             ||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
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RESULT 13
ABN86689
ID   ABN86689 standard; DNA; 12110 BP.
XX
AC   ABN86689;
XX
DT   05-NOV-2002 (first entry)

XX
DE Nucleotide sequence of vector Sinrep5-E7-Hsp70.
XX
KW Major histocompatibility complex; MHC; antigen presenting cell; APC;
KW antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic;
KW cancer; viral infection; HPV; E7; heat shock protein 70; Hsp70; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 7715. .9819
FT /*tag= a
FT /note= "E7-Hsp70 fusion sequence"
XX
PN WO200261113-A2.
XX
PD 08-AUG-2002.
XX
PF 01-FEB-2002; 2002WO-US002598.
XX
PR 01-FEB-2001; 2001US-0265334P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-619261/66.
XX
PT Nucleic acid molecule encoding a fusion polypeptide that promotes
PT processing via the Major Histocompatibility Complex class I pathway
PT and/or promotes activity of an antigen presenting cell, useful as vaccine
PT for cancer and viral infections.
XX
PS Claim 36; Page 30-33; 127pp; English.
XX
CC The invention relates to a new nucleic acid molecule (I) encoding a
CC fusion polypeptide useful as a vaccine composition. (I) comprises a first
CC nucleic acid sequence encoding a first polypeptide or peptide that
CC promotes processing via the Major Histocompatibility Complex (MHC) class
CC I pathway (MHC-I-PP) and/or promotes development or activity of an
CC antigen presenting cell (APC). The second nucleic acid sequence is linked
CC in frame to the first nucleic acid sequence or to a linker nucleic acid
CC sequence and encodes an antigenic polypeptide or peptide. The methods and
CC compositions of the present invention are useful as therapeutic vaccine
CC for cancer and for major viral infections, such as hepatoma and cervical
CC cancer, that cause morbidity and mortality. They can also be used in
CC treating animal diseases, such as equine herpesvirus, bovine viruses,
CC Marek's disease, retroviral and lentiviral diseases and rabies, in the
CC veterinary medicine context. The present sequence represents the
CC nucleotide sequence of vector Sinrep5-E7-Hsp70 comprising the human
CC papillomavirus (HPV) E7 antigenic protein and M. tuberculosis heat shock
CC protein 70 (Hsp70) fusion sequence
XX
SQ Sequence 12110 BP; 3339 A; 3084 C; 3137 G; 2550 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 6; Length 12110;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320
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Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400
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Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy         4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy         4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy         4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy         4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780

Qy         4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy         4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
                |||||||  | ||| |||||||||||||||||||||||||||||||||||||||||||||
Db         3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy         4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy         4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy         4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy         4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy         5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

Qy         5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260

Qy         5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy         5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380

Qy         5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy         5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500

Qy         5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy         5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy         5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy         5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

Qy         5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800

Qy         5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860

Qy         5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920

Qy         5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980

Qy         5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040

Qy         5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100

Qy         5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160

Qy         6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220

Qy         6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy         6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340

Qy         6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400

Qy         6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460

Qy         6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCCGCCAGG 6412
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCCGCCAGG 5520

Qy         6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580

Qy         6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640

Qy         6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
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Qy       6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760

Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880

Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| ||||
Db       6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780
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Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020

Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140

Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             ||||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
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RESULT 14
AAX77358
ID AAX77358 standard; DNA; 13905 BP.
XX
AC AAX77358;
XX
DT 09-AUG-1999 (first entry)
XX
DE Polynucleotide sequence of pTE5'2J.
XX
KW Nucleic acid identification; exogenous protein; gene sorting;
KW growth factor; membrane receptor; sindbis virus; ss.

XX
OS Synthetic.
XX
PN WO9925876-A1.
XX
PD 27-MAY-1999.
XX
PF 17-NOV-1998; 98WO-US024520.
XX
PR 17-NOV-1997; 97US-00972218.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
PI Bailey JE, Renner WA, Orberger GH, Koller D;
XX
DR WPI; 1999-357620/30.
XX
PT Isolating genes encoding proteins with selected properties, useful for
PT identifying therapeutic agents or targets.
XX
PS Disclosure; Fig 12A-D; 136pp; English.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing a population of eukaryotic host cells, culturing the
CC cells under suitable conditions and identifying cells that contain the
CC recombinant nucleic acid. The method is used to sort genes according to
CC the type of proteins they express, and also to identify new ligand/
CC receptor interactions. Typical applications of the nucleic acid and the
CC exogenous protein are in isolation of new growth factors, cytokines,
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
CC which may be useful as therapeutic agents or therapeutic targets, e.g.
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
CC proliferation or metabolic processes etc. The protein can also be used to
CC screen for specific modulators. The nucleic acid can also be used as
CC sources of therapeutic antisense or ribozyme sequences. The method allows
CC the protein (rather than a partial DNA sequence) to be isolated and,
CC since a wide range of cells can be used, they can be expressed with the
CC correct glycosylation pattern
XX
SQ Sequence 13905 BP; 3931 A; 3551 C; 3440 G; 2983 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 2; Length 13905;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500
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Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy       2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy       2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy       2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 1800

Qy       2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 1860

Qy       2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920

Qy       2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980

Qy       2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy       2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy       2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 2160

Qy       3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 2220

Qy       3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy       3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy       3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

Qy       3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy       3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy       3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy       3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy       3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700

Qy       3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy       3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy       3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy       3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy       3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3000

Qy       3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy       3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy       4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy       4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy       4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy       4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy       4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy       4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy       4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy       4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy       4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy       4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720
Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
Db      3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780
Qy      4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
Db      3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840
Qy      4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
Db      3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900
Qy      4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
Db      3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960
Qy      4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
Db      3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020
Qy      4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
Db      4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080
Qy      4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
Db      4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140
Qy      5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
Db      4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200
Qy      5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
Db      4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260
Qy      5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
Db      4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320
Qy      5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
Db      4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380
Qy      5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
Db      4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440
Qy      5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
Db      4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500
Qy      5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
Db      4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560
Qy      5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
Db      4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620
Qy      5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
Db      4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680
Qy      5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
Db      4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740
Qy      5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
Db      4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800
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Qy      5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
Db      4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860
Qy      5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db      4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920
Qy      5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
Db      4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980
Qy      5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
Db      4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040
Qy      5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
Db      5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100
Qy      5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
Db      5101 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 5160
Qy      6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
Db      5161 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 5220
Qy      6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
Db      5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280
Qy      6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
Db      5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340
Qy      6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
Db      5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400
Qy      6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
Db      5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460
Qy      6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
Db      5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520
Qy      6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
Db      5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580
Qy      6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
Db      5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640
Qy      6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
Db      5641 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 5700
Qy      6593 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 6652
Db      5701 CACTACGCAAGCAGAGACGTAGACGCAGGAGCAGGAGGACTGAATACTGACTAACCGGGG 5760
Qy      6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
Db      5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820
Qy      6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
Db      5821 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 5880
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Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
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Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

Qy       6893 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 AGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATCAGCCAGAATGCTATA 6060

Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 6120

Qy       7013 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 AGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180

Qy       7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCGCATGCC 7132
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||
Db       6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGGGACAGTCGCCTGCC 6240

Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420

Qy       7313 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 7372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 ACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCATGTAATGACGAGTATTGGG 6480

Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 6660

Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 6780

Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6841 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 6900

Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 6960

Qy       7853 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7912
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Db       6961 CACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCATCCACCCATCTACCTACGG 7020

Qy       7913 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7972
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Db       7021 GTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCCTCACACTTTTTGTCA 7080

Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 7140

Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7141 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 7200

Qy       8093 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 8152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7201 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGATCATCGACGCAGTCATCG 7260

Qy       8153 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 8212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7261 GTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG 7320

Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

Qy       8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 8512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGTCAGCATAGTACATTTCAT 7620

Qy       8513 CTGACTAATACTACAACACCACCACCT 8539
             |||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
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RESULT 15
AAA90390
ID AAA90390 standard; DNA; 13905 BP.
XX
AC AAA90390;
XX
DT 10-JAN-2001 (first entry)
XX
DE Plasmid pTE5'2J DNA sequence.
XX
KW Nucleic acid identification; exogenous protein; drug screening;
KW recombinant expression; pTE5'2J; cyclic; circular; ds.
XX
OS Synthetic.
XX
PN JP2000189173-A.
XX
PD 11-JUL-2000.
XX
PF 23-AUG-1999; 99JP-00236220.
XX
PR 17-NOV-1998; 98US-00193707.
PR 17-NOV-1998; 98WO-US024520.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.

XX
DR WPI; 2000-551637/51.
XX
PT Identifying a recombinant nucleic acid to identify and isolate various
PT cellular proteins, comprises culturing a composition comprising
PT eukaryotic host cells and identifying a cell comprising recombinant
PT nucleic acid.
XX
PS Example; Fig 12A-D; 56pp; Japanese.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property.The method
CC comprises preparing populations of eukaryotic host cells, where each cell
CC comprises an expression vector encoding a different exogenous protein.
CC The host cells are cultured under suitable conditions and the nucleic
CC acid which encodes the exogenous protein is identified. The method is
CC useful for the identification and isolation of proteins with a selected
CC property. Typical applications of the nucleic acid and the exogenous
CC protein are in isolation of new growth factors, cytokines, membrane
CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may
CC be useful as therapeutic agents or therapeutic targets, e.g., pro-
CC apoptotic or tumour suppressing proteins, regulators of cell
CC proliferation or of metabolic processes. The protein can also be used to
CC screen for ligands and specific modulators of activity. The method of the
CC invention allows the direct cloning of full length cDNAs in one step. It
CC facilitates direct expression of the protein without the need to perform
CC further procedures such as subcloning and establishment of a cell line
CC for protein production. The method allows a protein of interest (rather
CC than a partial DNA sequence) to be isolated and, since a wide range of
CC cell types can be used, they can be expressed in a correctly folded and
CC glycosylated form. The present sequence represents plasmid pTE5'2J which
CC was used in the exemplifications of the invention. This patent is related
CC to WO9925876
XX
SQ Sequence 13905 BP; 3931 A; 3551 C; 3440 G; 2983 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 3; Length 13905;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        893 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTGACGGCGTAGTACACACTATTGAATCAAACAGCCGACCAATTGCACTACCATCACAA 60

Qy        953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGC 120

Qy       1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTA 180

Qy       1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAG 240

Qy       1133 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC 300

Qy       1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTA 360

Qy       1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATC 420

Qy       1313 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCGGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATG 480

Qy       1373 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTATATCAACGCTCCCG 540

Qy       1433 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 1492
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Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy       1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy       1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy       1613 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 1672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy       1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy       1733 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 1792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy       1793 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 1852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy       1853 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1913 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1973 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 2032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       2033 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 2092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2093 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 2152
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Qy       2153 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
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Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

Qy       2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 2272
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Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

Qy       2273 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 2332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

Qy       2333 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 2392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGCCCATGTCGCTGAGGCAGAAATTGAAACTGGCATTGCAACCAAAGAAGGAGGAAAAAC 1500

Qy       2393 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 2452
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Qy       2453 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 2512
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Db      1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

Qy      2513 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 2572
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Db      1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy      2573 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 2632
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Db      1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy      2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAAACTCGCACCAG 2692
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Qy      2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATAACACACTCCGGAAGATCAGGAAGGTACG 2752
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Qy      2753 CGGTCGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
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Qy      2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 2872
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Db      1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTTGTGAACC 1980

Qy      2873 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 GCAAACTATACCACATTGCCATGCATGGCCCCGCCAAGAATACAGAAGAGGAGCAGTACA 2040

Qy      2933 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 AGGTTACAAAGGCAGAGCTTGCAGAAACAGAGTACGTGTTTGACGTGGACAAGAAGCGTT 2100

Qy      2993 GCGTTAAGAAGGAAGAAGCCTCAGGTCTGGTCCTCTCGGGAGAACTGACCAACCCTCCCT 3052
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Qy      3053 ATCATGAGCTAGCTCTGGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAGGTCGAAA 3112
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Qy      3113 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
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Db      2221 CAATAGGAGTGATAGGCACACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA 2280

Qy      3173 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 3232
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 CGGCACGAGATCTTGTTACCAGCGGAAAGAAAGAAAATTGTCGCGAAATTGAGGCCGACG 2340

Qy      3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
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Db      2341 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400

Qy      3293 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 3352
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Db      2401 GATGCCACAAAGCCGTAGAAGTGCTGTACGTTGACGAAGCGTTCGCGTGCCACGCAGGAG 2460

Qy      3353 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 3412
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Db      2461 CACTACTTGCCTTGATTGCTATCGTCAGGCCCCGCAAGAAGGTAGTACTATGCGGAGACC 2520

Qy      3413 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 3472
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Db      2521 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCTGAAA 2580

Qy      3473 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 3532
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Db      2581 AAGACATATGCACCAAGACATTCTACAAGTATATCTCCCGGCGTTGCACACAGCCAGTTA 2640

Qy      3533 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 3592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAAACCACGAACCCGTGCAAGA 2700
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Qy      3593 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 3652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCCTGA 2760

Qy      3653 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 3712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAATCGACTATCCCGGACATGAAGTAATGA 2820

Qy      3713 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 CAGCCGCGGCCTCACAAGGGCTAACCAGAAAAGGAGTGTATGCCGTCCGGCAAAAAGTCA 2880

Qy      3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 3832
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Db      2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTTGCTCACCCGCACTG 2940

Qy      3833 AGGACAGGCTAGTGTGGAAAACCTTGCAGGGCGACCCATGGATTAAGCAGCCCACTAACA 3892
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Qy      3893 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 TACCTAAAGGAAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATAA 3060

Qy      3953 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 4012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 TTGCTGCAATAAACAGCCCCACTCCCCGTGCCAATCCGTTCAGCTGCAAGACCAACGTTT 3120

Qy      4013 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 4072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 GCTGGGCGAAAGCATTGGAACCGATACTAGCCACGGCCGGTATCGTACTTACCGGTTGCC 3180

Qy      4073 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 4132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 AGTGGAGCGAACTGTTCCCACAGTTTGCGGATGACAAACCACATTCGGCCATTTACGCCT 3240

Qy      4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 4192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGGACTTGACAAGCGGACTGTTTTCTAAAC 3300

Qy      4193 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 4252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 AGAGCATCCCACTAACGTACCATCCCGCCGATTCAGCGAGGCCGGTAGCTCATTGGGACA 3360

Qy      4253 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 4312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 ACAGCCCAGGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACTCTCCCGTA 3420

Qy      4313 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 4372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GATTTCCGGTGTTCCAGCTAGCTGGGAAGGGCACACAACTTGATTTGCAGACGGGGAGAA 3480

Qy      4373 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 4432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 CCAGAGTTATCTCTGCACAGCATAACCTGGTCCCGGTGAACCGCAATCTTCCTCACGCCT 3540

Qy      4433 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 4492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 TAGTCCCCGAGTACAAGGAGAAGCAACCCGGCCCGGTCAAAAAATTCTTGAACCAGTTCA 3600

Qy      4493 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 4552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 AACACCACTCAGTACTTGTGGTATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAATCG 3660

Qy      4553 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 4612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 AATGGATCGCCCCGATTGGCATAGCCGGTGCAGATAAGAACTACAACCTGGCTTTCGGGT 3720

Qy      4613 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 4672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 TTCCGCCGCAGGCACGGTACGACCTGGTGTTCATCAACATTGGAACTAAATACAGAAACC 3780
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Qy       4673 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 4732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 ACCACTTTCAGCAGTGCGAAGACCATGCGGCGACCTTAAAAACCCTTTCGCGTTCGGCCC 3840

Qy       4733 TGAATTGTTTAAACTCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 4792
             ||||||| | ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGAATTGCCTTAACCCAGGAGGCACCCTCGTGGTGAAGTCCTATGGCTACGCCGACCGCA 3900

Qy       4793 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 4852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 ACAGTGAGGACGTAGTCACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGAC 3960

Qy       4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTTCCGACAACTAGACAACAGCC 4020

Qy       4913 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 GTACACGGCAATTCACCCCGCACCATCTGAATTGCGTGATTTCGTCCGTGTATGAGGGTA 4080

Qy       4973 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 5032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CAAGAGATGGAGTTGGAGCCGCGCCGTCATACCGCACCAAAAGGGAGAATATTGCTGACT 4140

Qy       5033 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 5092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 GTCAAGAGGAAGCAGTTGTCAACGCAGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT 4200

Qy       5093 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 5152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 GCCGTGCCATCTATAAACGTTGGCCGACCAGTTTTACCGATTCAGCCACGGAGACAGGCA 4260

Qy       5153 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 5212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCTGATTTCC 4320

Qy       5213 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 5272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GGAAGCACCCAGAAGCAGAAGCCTTGAAATTGCTACAAAACGCCTACCATGCAGTGGCAG 4380

Qy       5273 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 5332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ACTTAGTAAATGAACATAACATCAAGTCTGTCGCCATTCCACTGCTATCTACAGGCATTT 4440

Qy       5333 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 5392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 ACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCGCTAGACA 4500

Qy       5393 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 5452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GAACTGACGCGGACGTAACCATCTATTGCCTGGATAAGAAGTGGAAGGAAAGAATCGACG 4560

Qy       5453 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 5512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 CGGCACTCCAACTTAAGGAGTCTGTAACAGAGCTGAAGGATGAAGATATGGAGATCGACG 4620

Qy       5513 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 5572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 ATGAGTTAGTATGGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGGATTCAGTACTA 4680

Qy       5573 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 5632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 CAAAAGGAAAATTGTATTCGTACTTCGAAGGCACCAAATTCCATCAAGCAGCAAAAGACA 4740

Qy       5633 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 5692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 TGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTGTGTGCCT 4800

Qy       5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 5752
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Db       4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCATAACCCGT 4860

Qy       5753 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 5812
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGG 4920

Qy       5813 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 5872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACCCCCCTTC 4980

Qy       5873 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5932
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Db       4981 CTAAGCACAAAATTAAGAATGTTCAGAAGGTTCAGTGCACGAAAGTAGTCCTGTTTAATC 5040

Qy       5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5992
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Db       5041 CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTGCCAGAACAGCCTACCG 5100

Qy       5993 CTCCTCCTGCACAGGCCGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCACCATCTACAG 6052
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Qy       6053 CTGATAACACCTCGCTTGATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
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Qy       6113 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 6172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCACTTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGGACAGTTGGT 5280

Qy       6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 6232
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Db       5281 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGCAGGTGGTGGTGGCTGACGTTC 5340

Qy       6233 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 6292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 ATGCCGTCCAAGAGCCTGCCCCTATTCCACCGCCAAGGCTAAAGAAGATGGCCCGCCTGG 5400

Qy       6293 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 6352
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Db       5401 CAGCGGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT 5460

Qy       6353 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 6412
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Db       5461 CTTTTGGTGGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCGCCAGG 5520

Qy       6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 6472
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Db       5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCGGATCGTTTT 5580

Qy       6473 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 6532
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Db       5581 CCGACGGAGAGATTGATGAGCTGAGCCGCAGAGTAACTGAGTCCGAACCCGTCCTGTTTG 5640

Qy       6533 GATCATTTGAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6653 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 6712
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Db       5761 TAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTTC 5820

Qy       6713 TGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAATTCATGCCC 6772
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Qy       6773 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 6832
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Db       5881 CGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACCAGATGATGCCCACCG 5940

Qy       6833 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6892
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Db       5941 AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAGCCATAACCACTG 6000

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Qy       6953 AGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
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Qy       7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 7192
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Db       6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAACATGAGTATA 6300

Qy       7193 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 7252
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Db       6301 GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAAATGTGC 6360

Qy       7253 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 7312
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Db       6361 TCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGCGTGAACTGCCAACACTGG 6420

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Qy       7373 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 7432
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Db       6481 AGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTGTCACCGCATATGTAGCTA 6540

Qy       7433 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 7492
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Db       6541 GACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGTATAATTTGGTCCCATTGC 6600

Qy       7493 AAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAGACGTGAAAGTTACACCAG 7552
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Qy       7553 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 7612
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Db       6661 GCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATACAAGCCGCAGAACCCCTGG 6720

Qy       7613 CGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTAGGCTTACGGCCGTCTTGC 7672
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Qy       7673 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 7732
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Db       6781 TTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATTTTGATGCAATCATAGCAG 6840

Qy       7733 AACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC 7792
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Qy       7793 AAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGGACCTGGGTGTGGATCAAC 7852
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Qy       7973 ACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACGTCCA 8032
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Qy       8033 GATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAGTAGTATCTGACAAAGAAA 8092
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Qy       8213 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 8272
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Db       7321 CGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCCAGCCG 7380

Qy       8273 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 8332
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Db       7381 ACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA 7440

Qy       8333 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 8392
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Db       7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA 7500

Qy       8393 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 8452
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Db       7501 TTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCAAAAGAGCATTCCAAGCCA 7560

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             ||||||||||||||||||||||||||||
Db       7621 CTGACTAATACTACAACACCACCACCT 7647
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Search completed: March 23, 2005, 12:34:32
Job time : 2714 secs